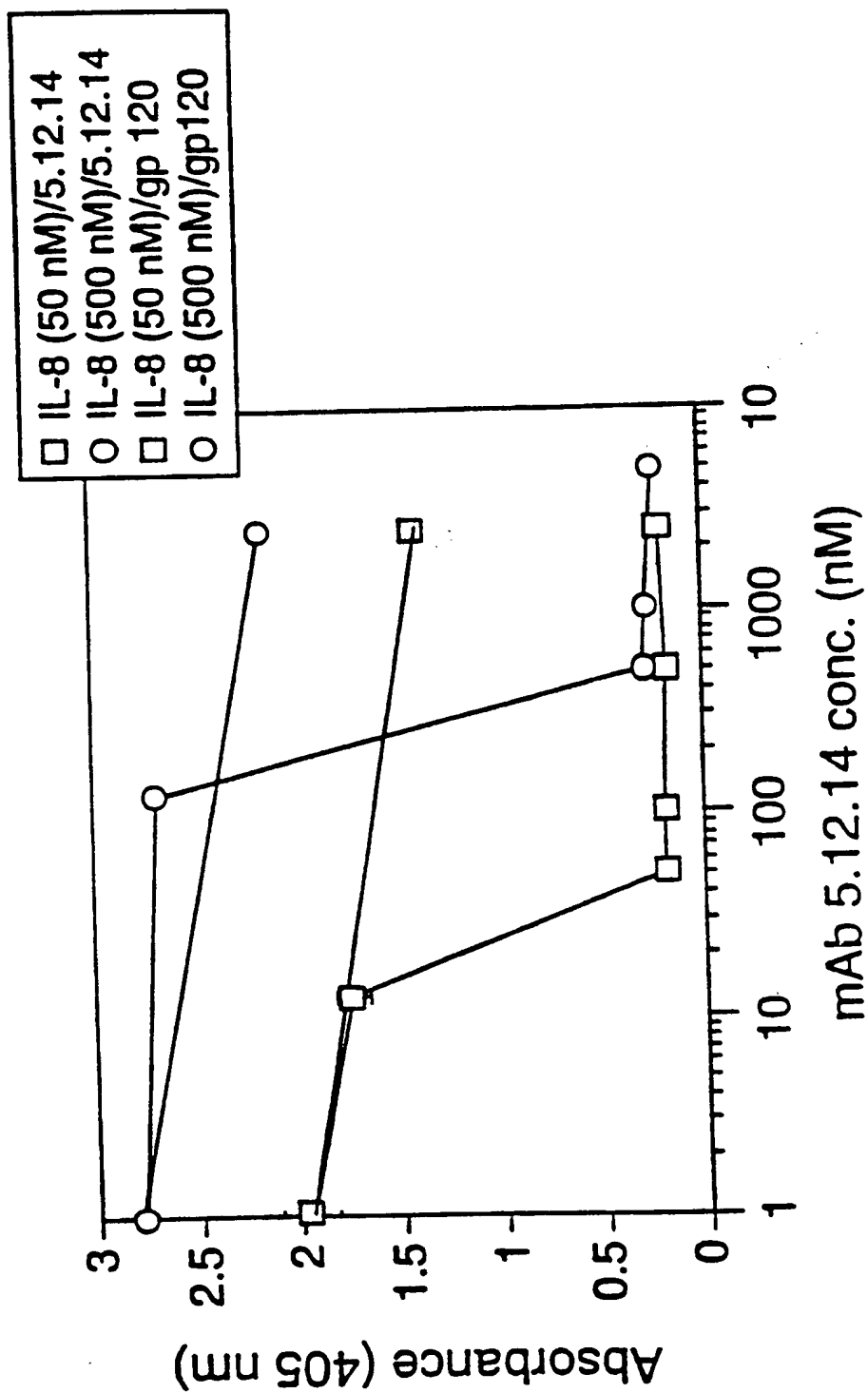
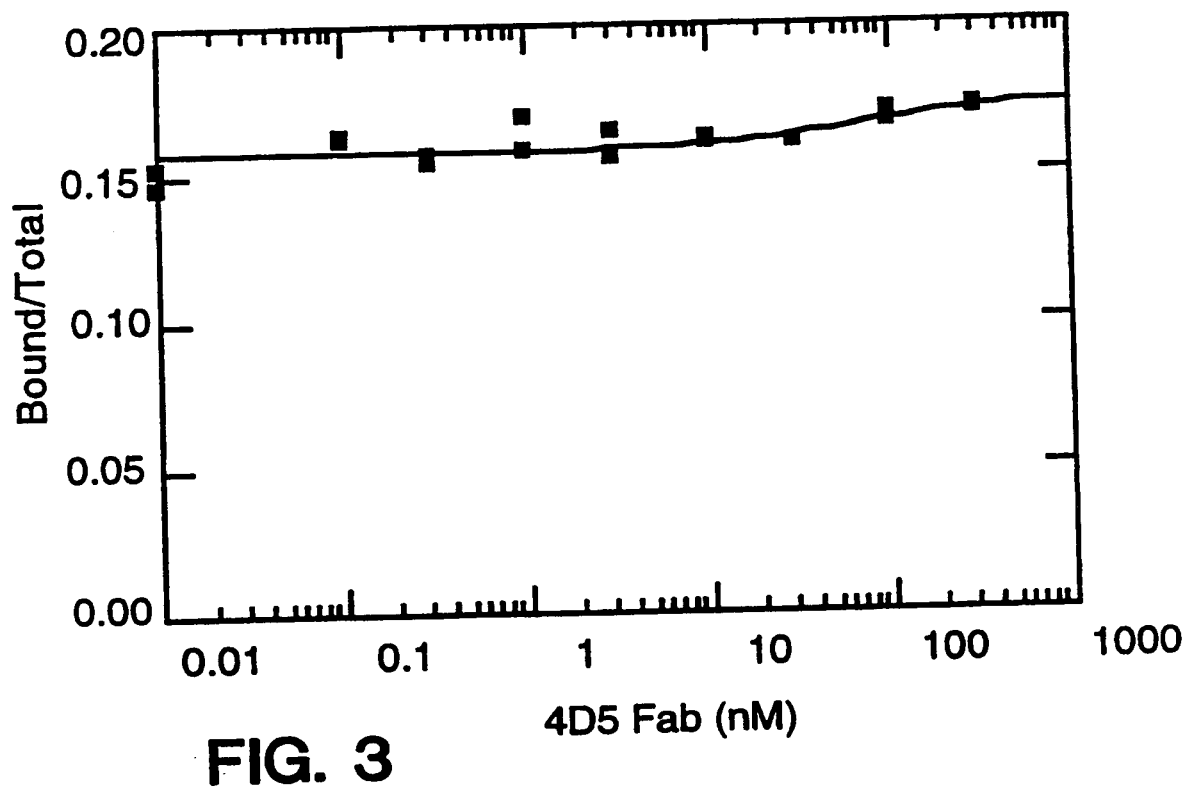
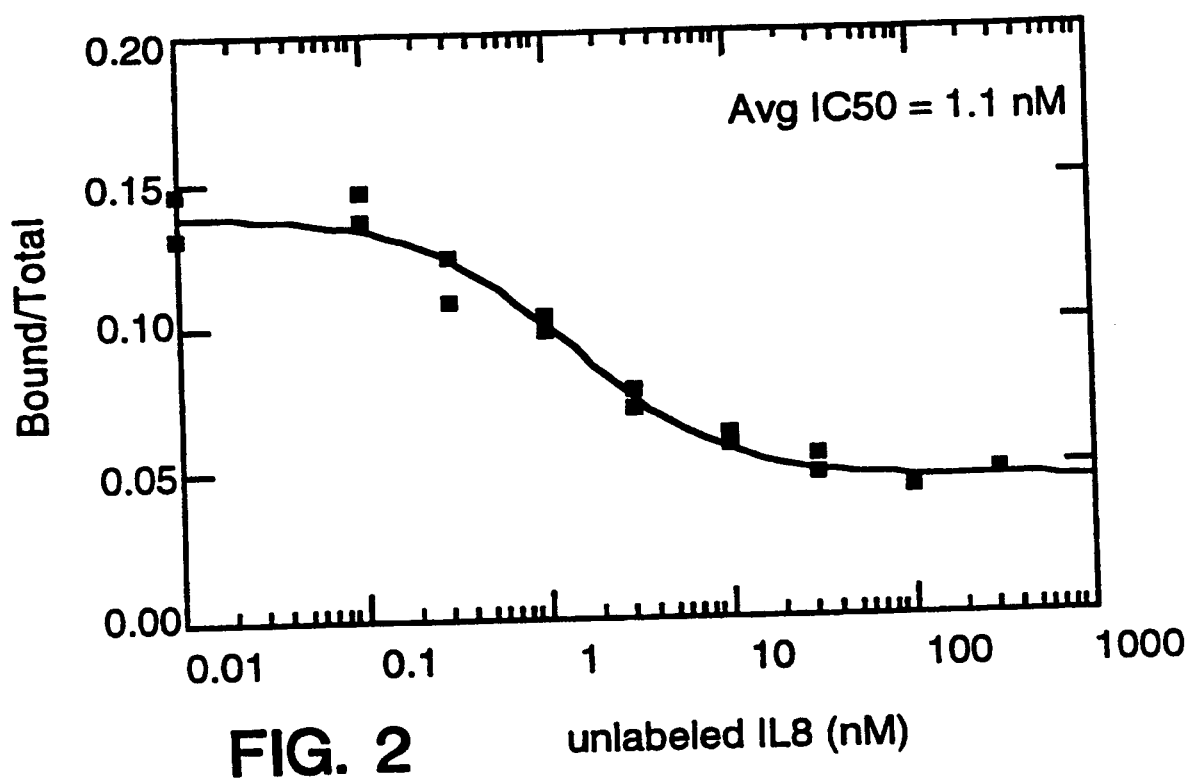


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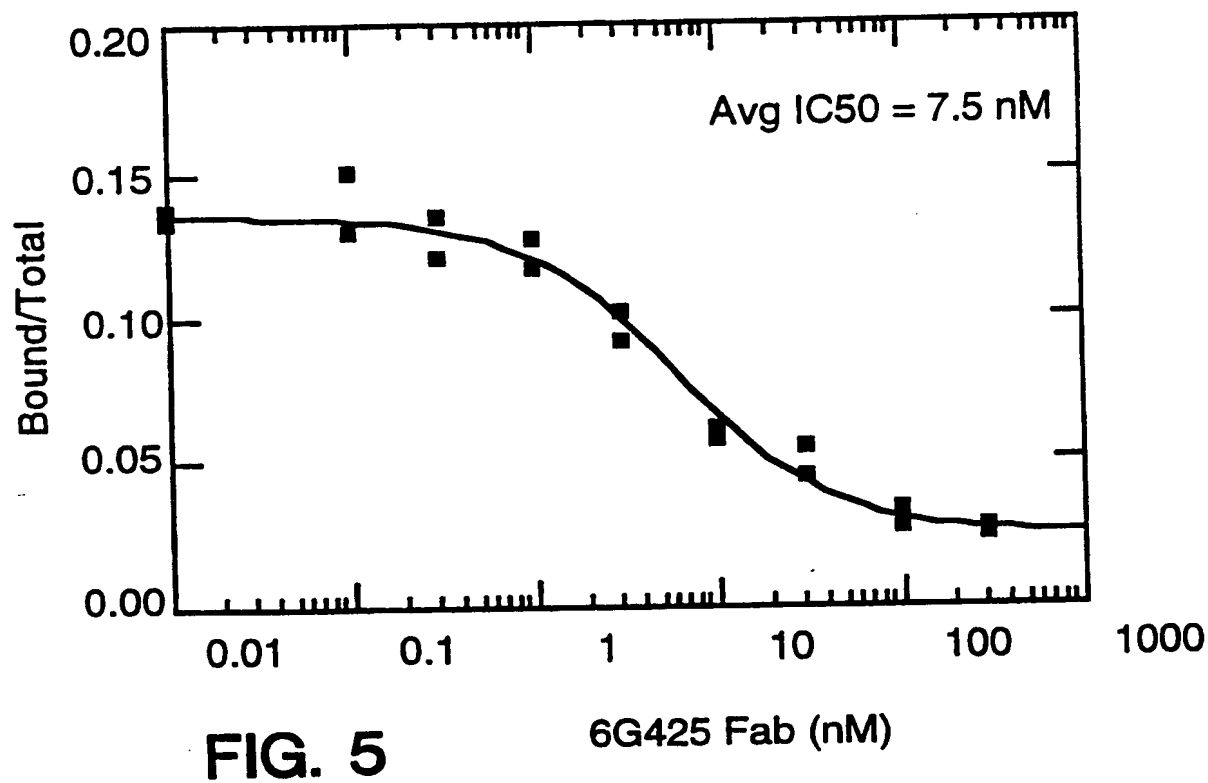
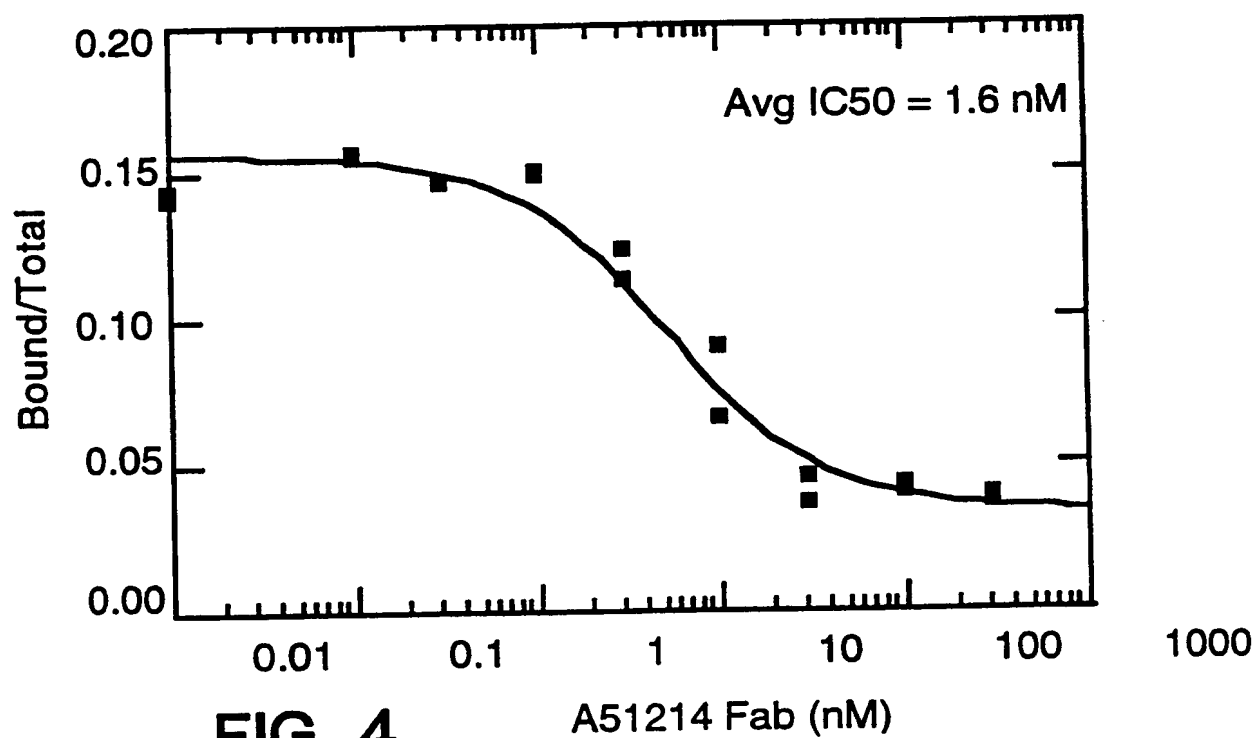
FIG. 1



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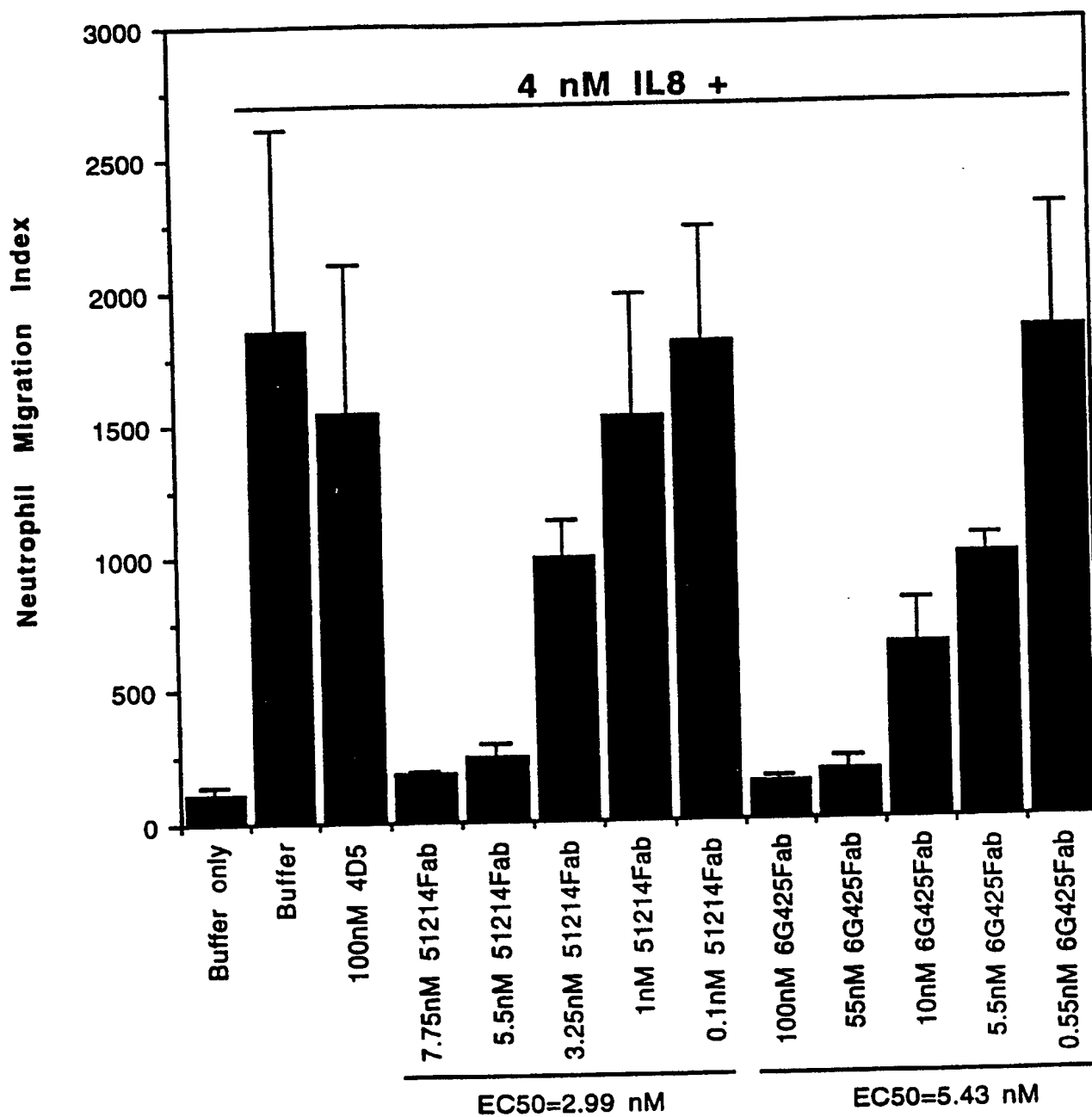


FIG. 6

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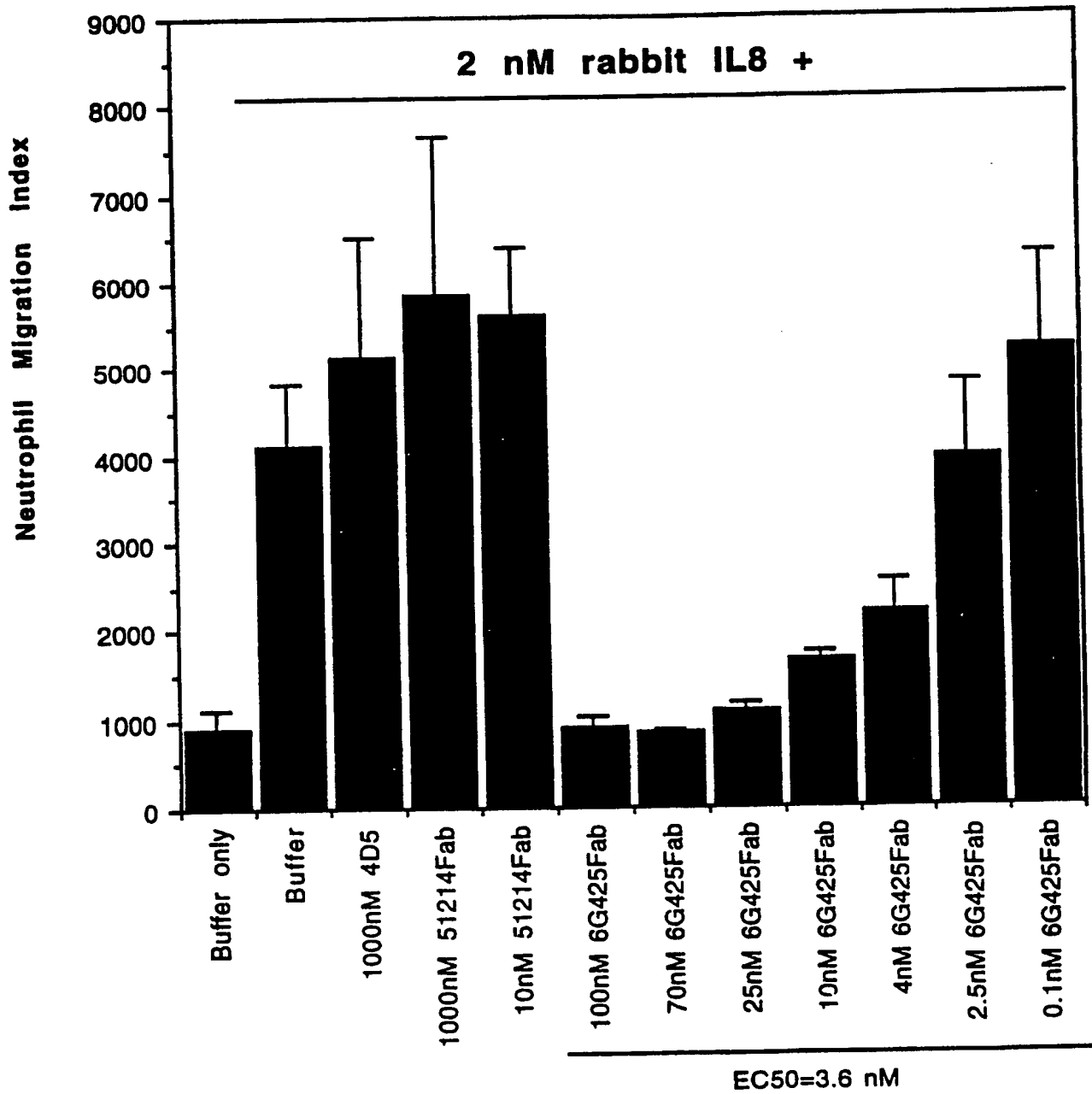


FIG. 7

FIG. 8

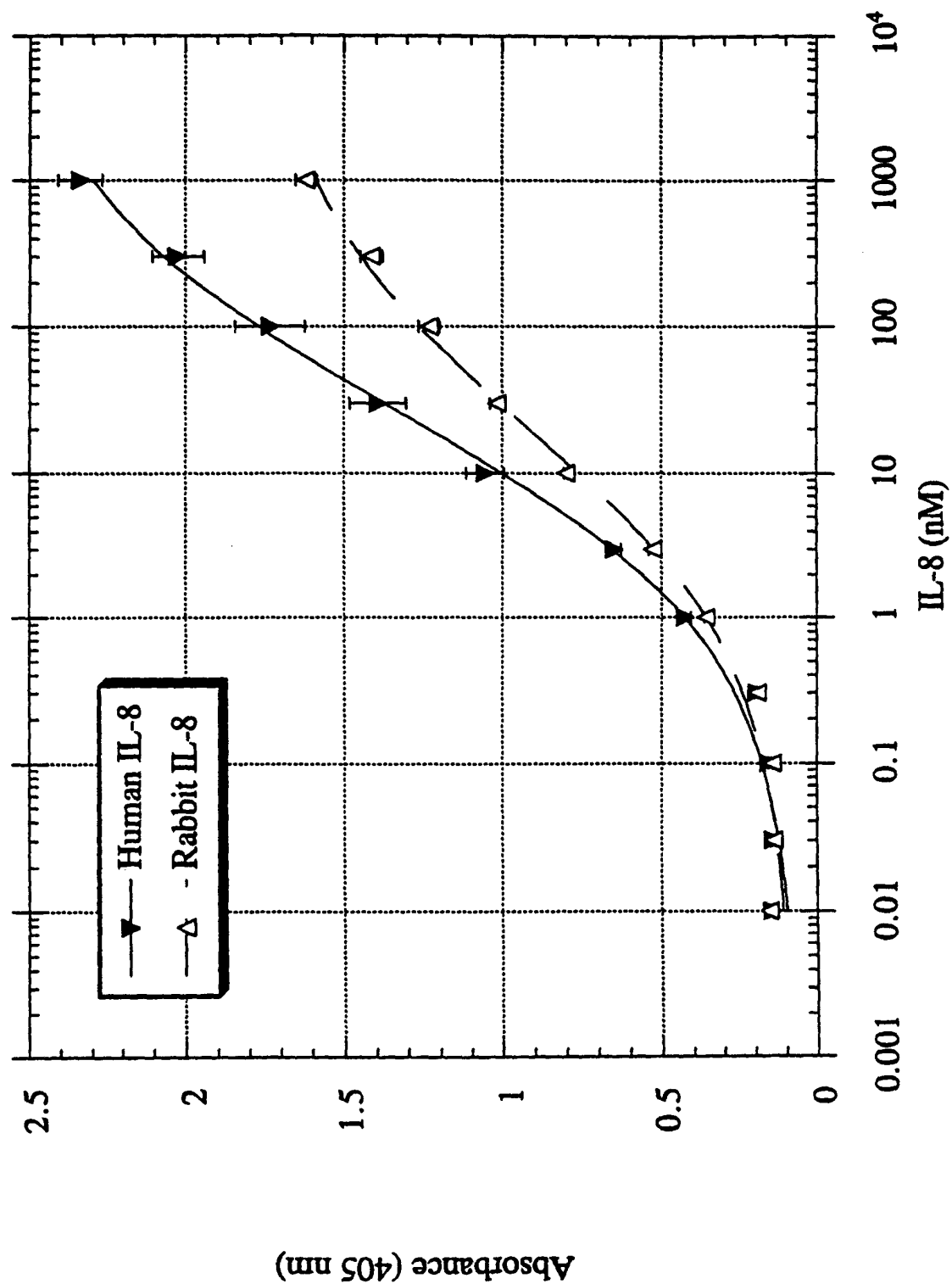


FIG. 9

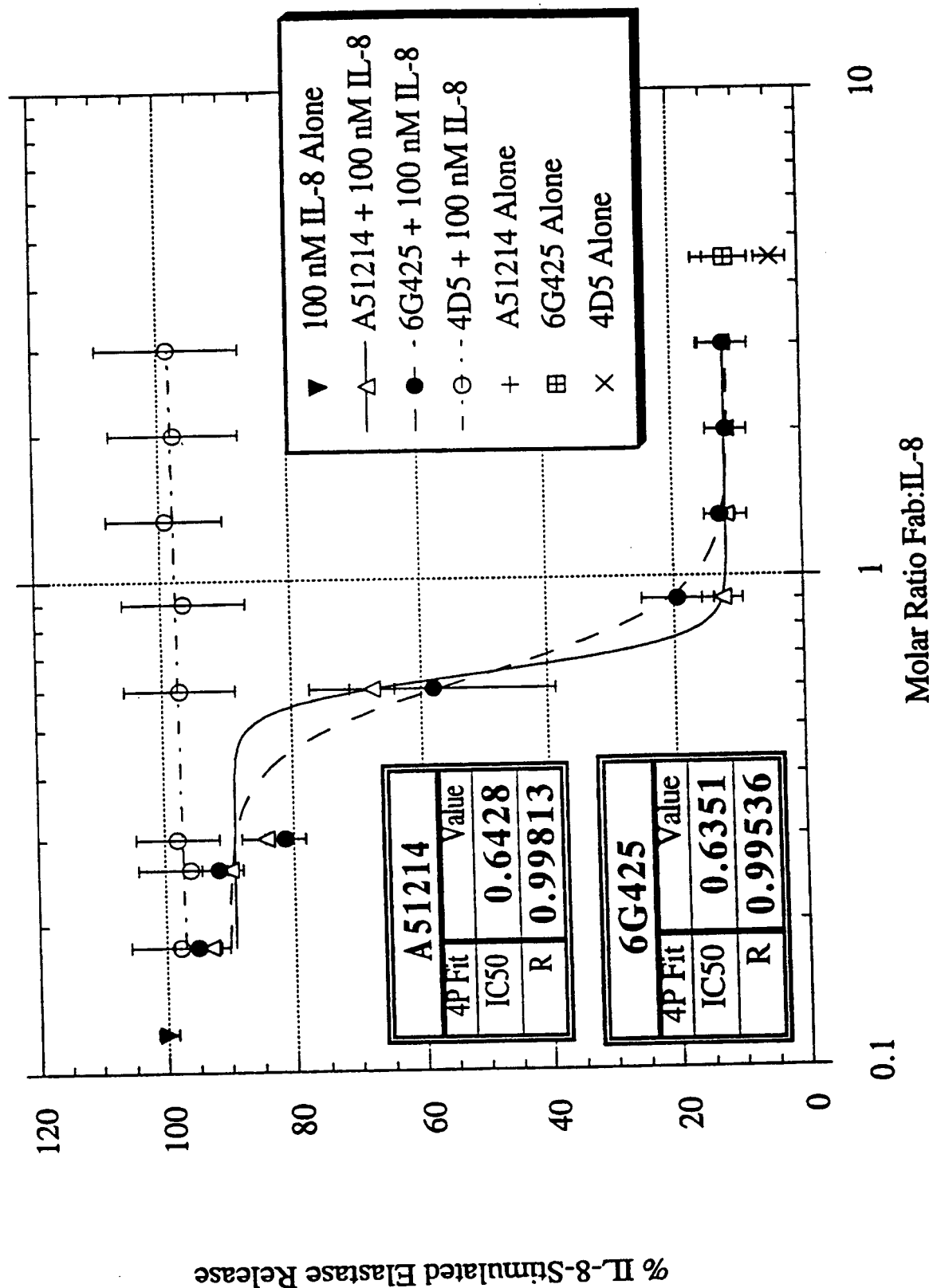
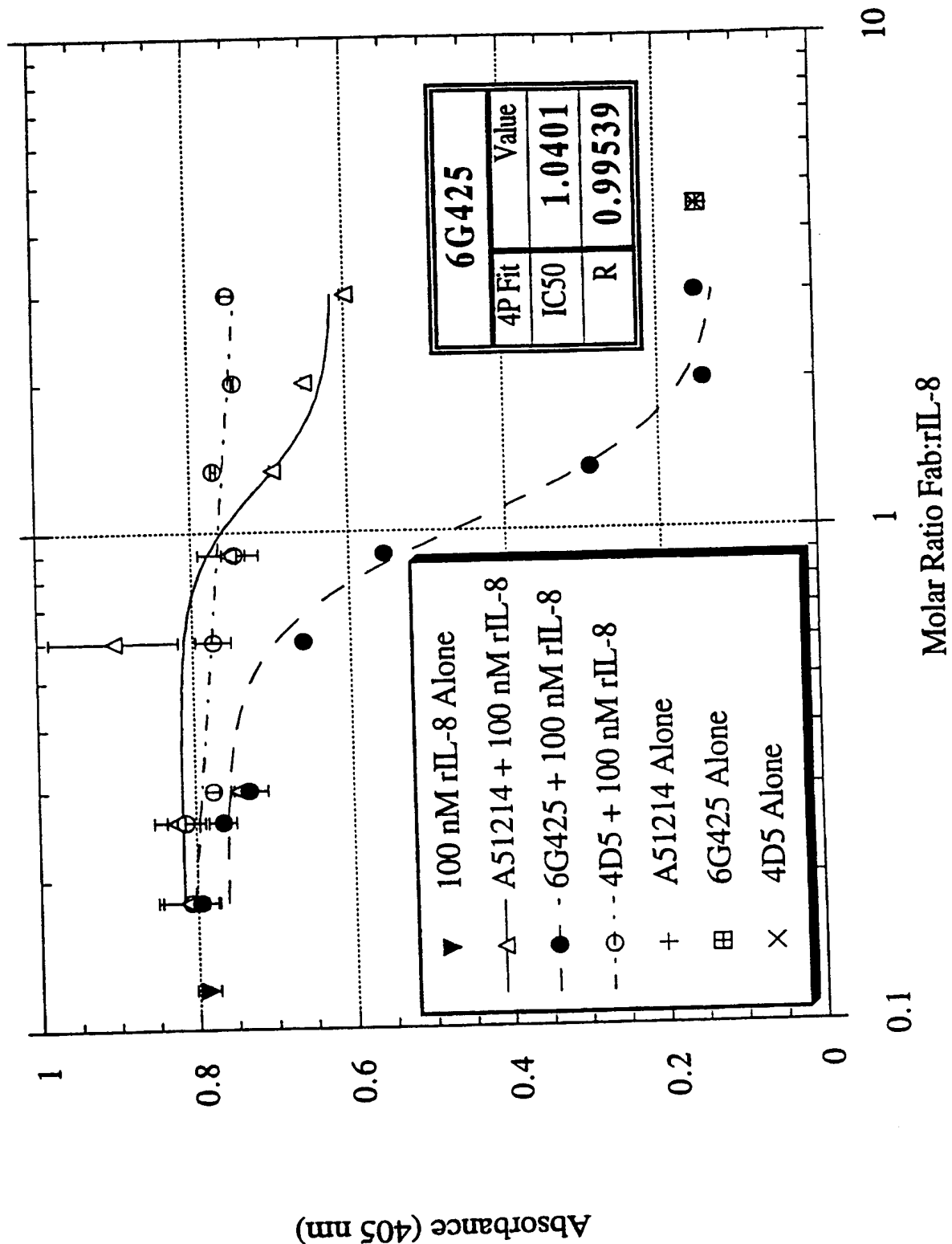


FIG. 10



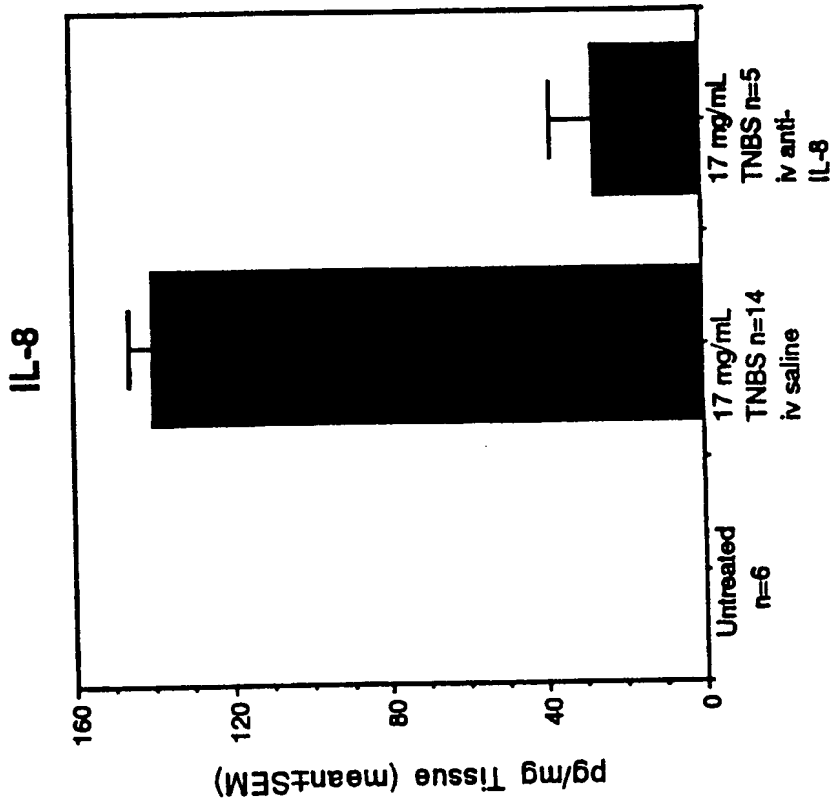


FIG. 11B

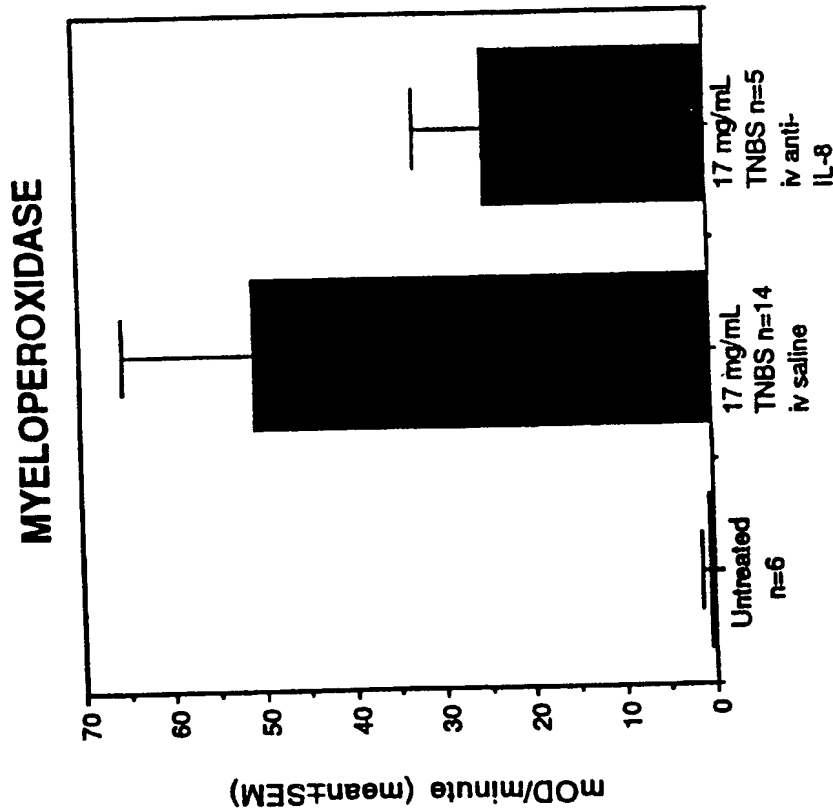


FIG. 11A

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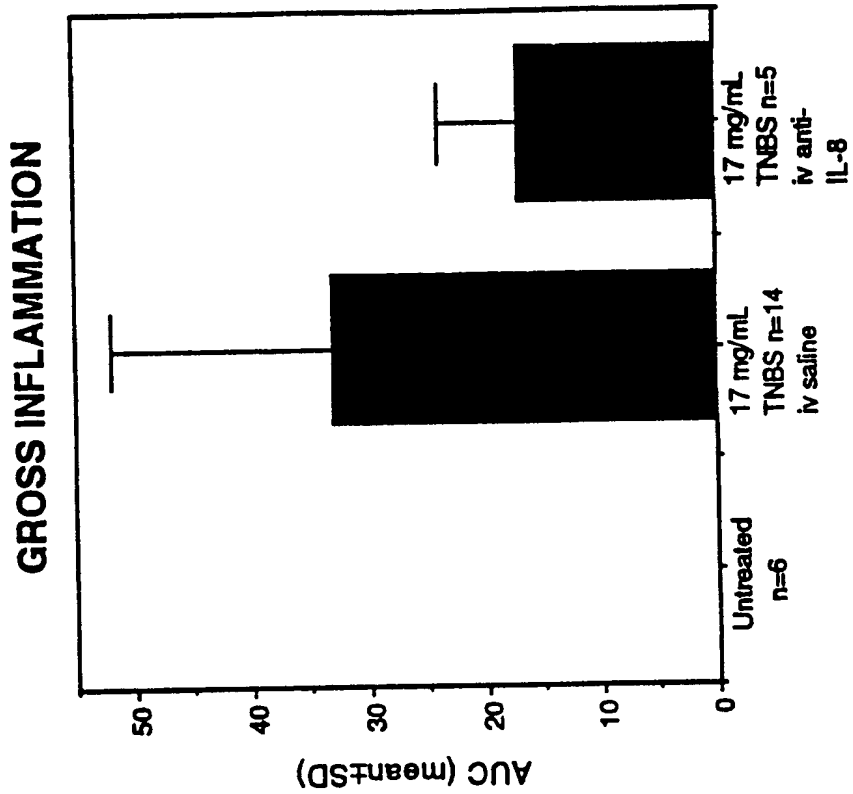


FIG. 11D

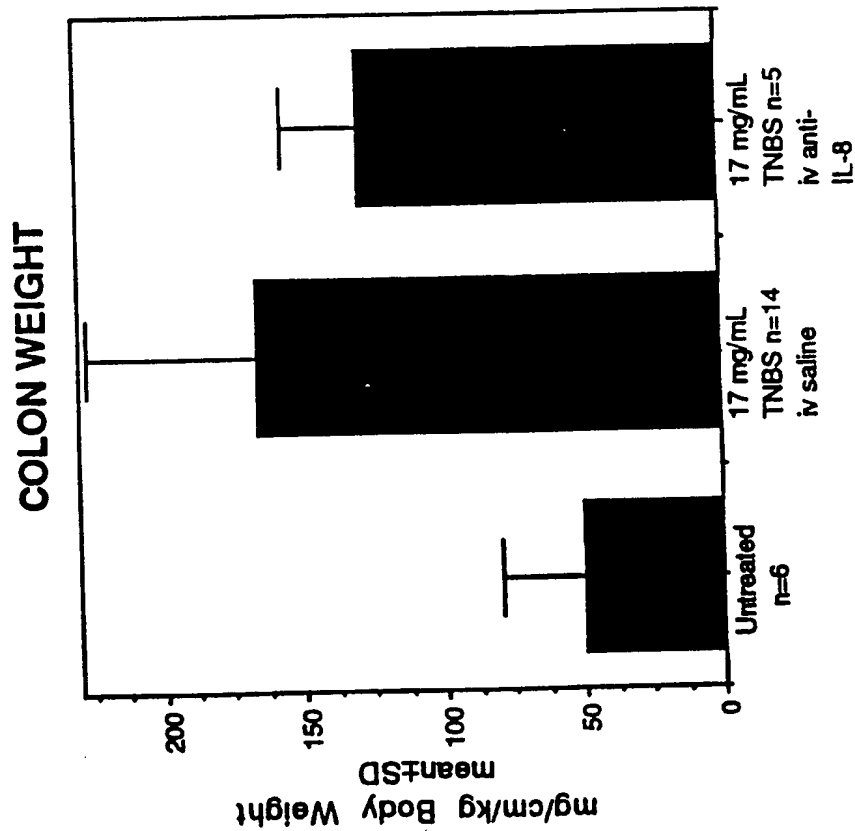


FIG. 11C

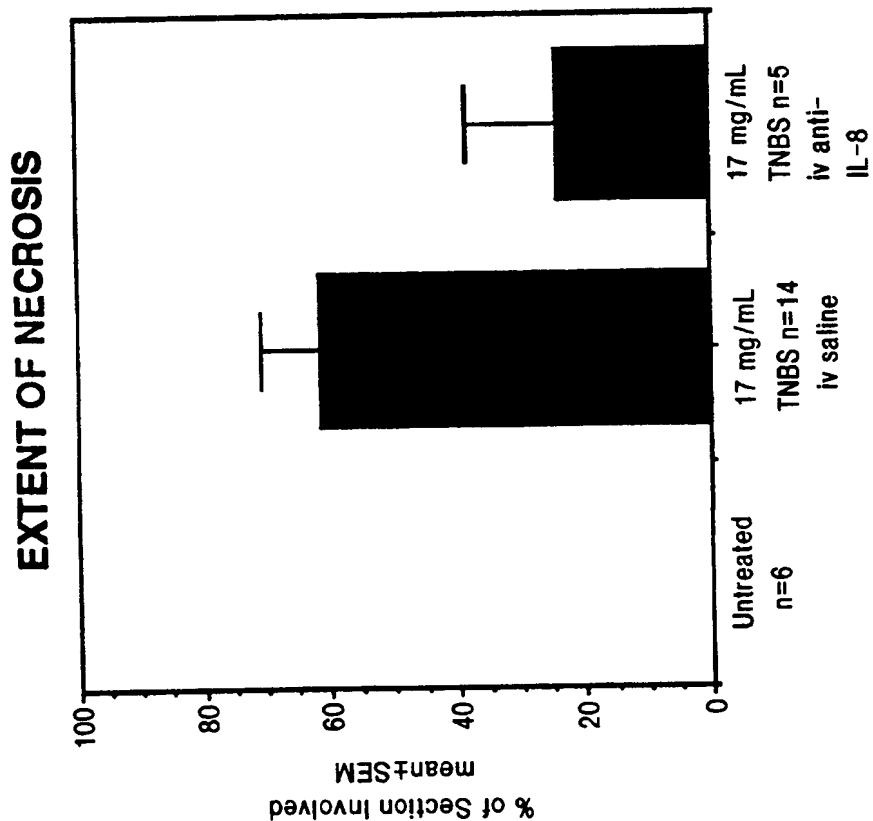


FIG. 11F

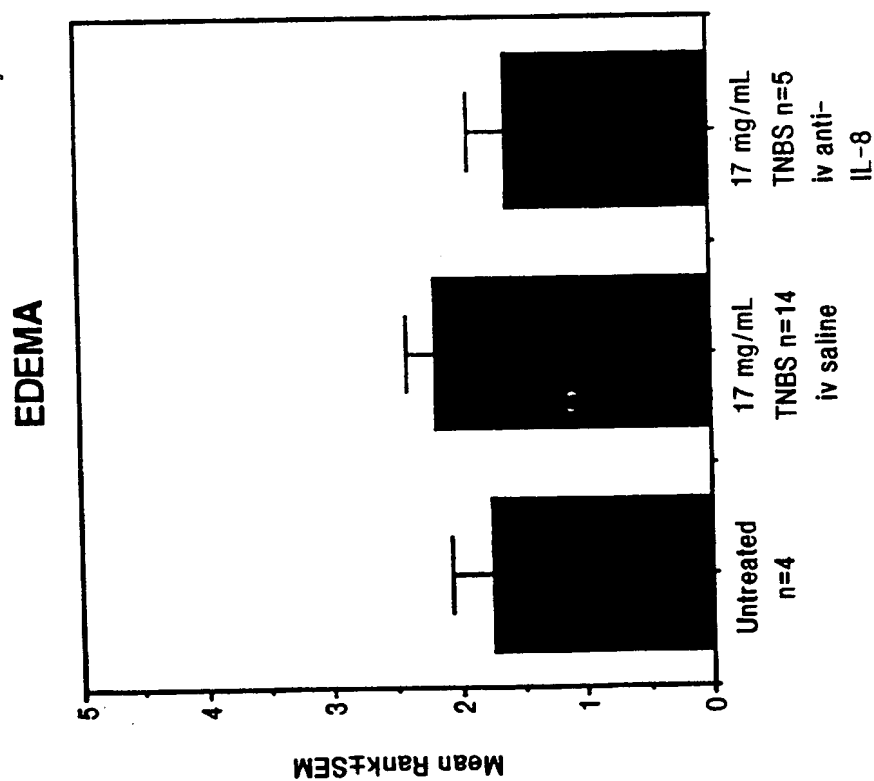


FIG. 11E

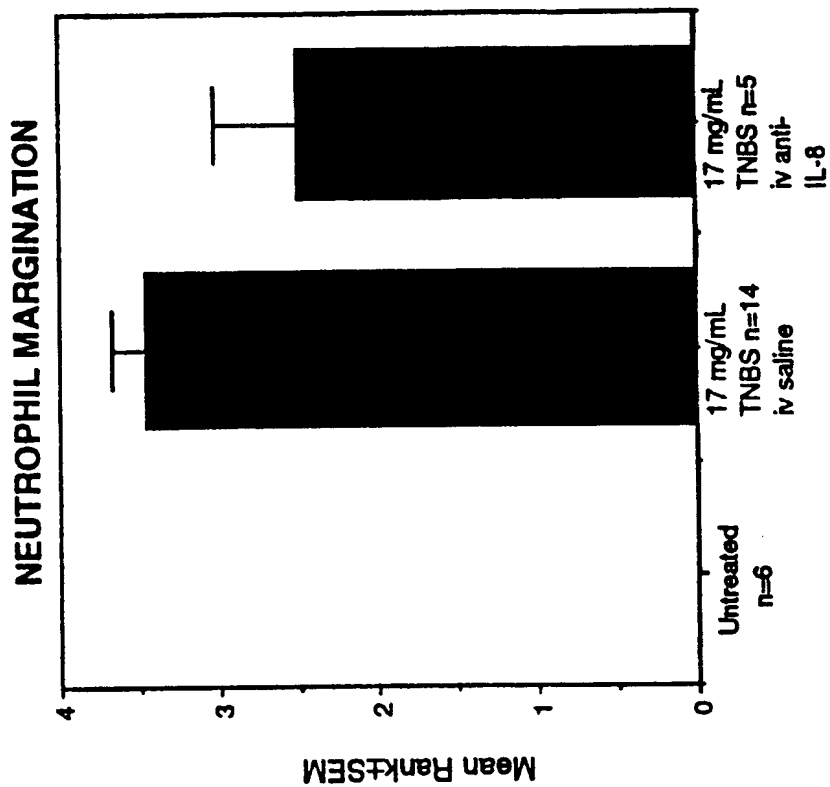


FIG. 11H

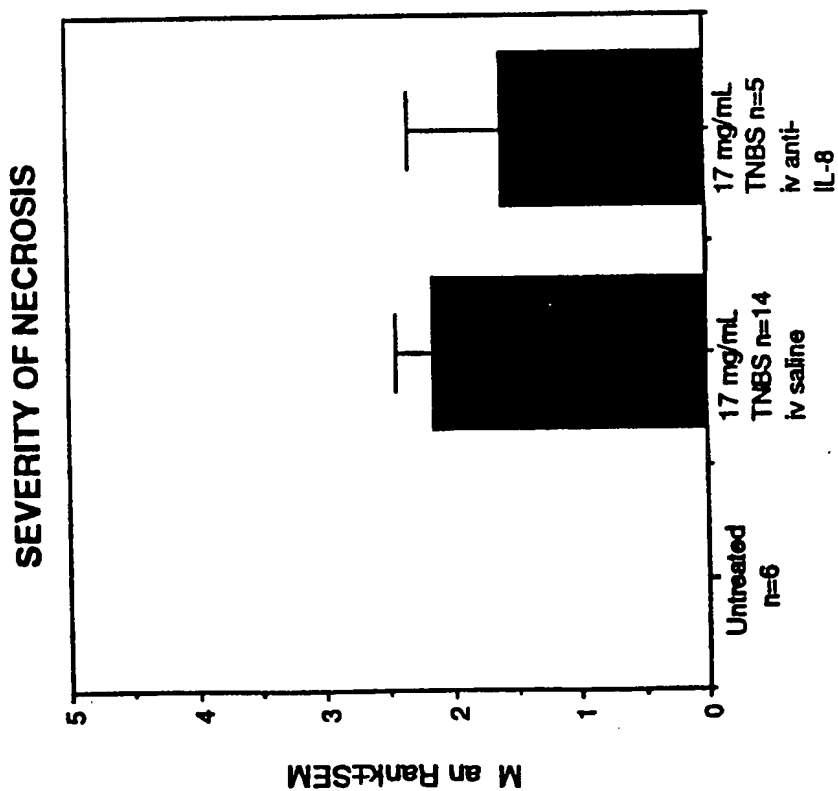


FIG. 11G

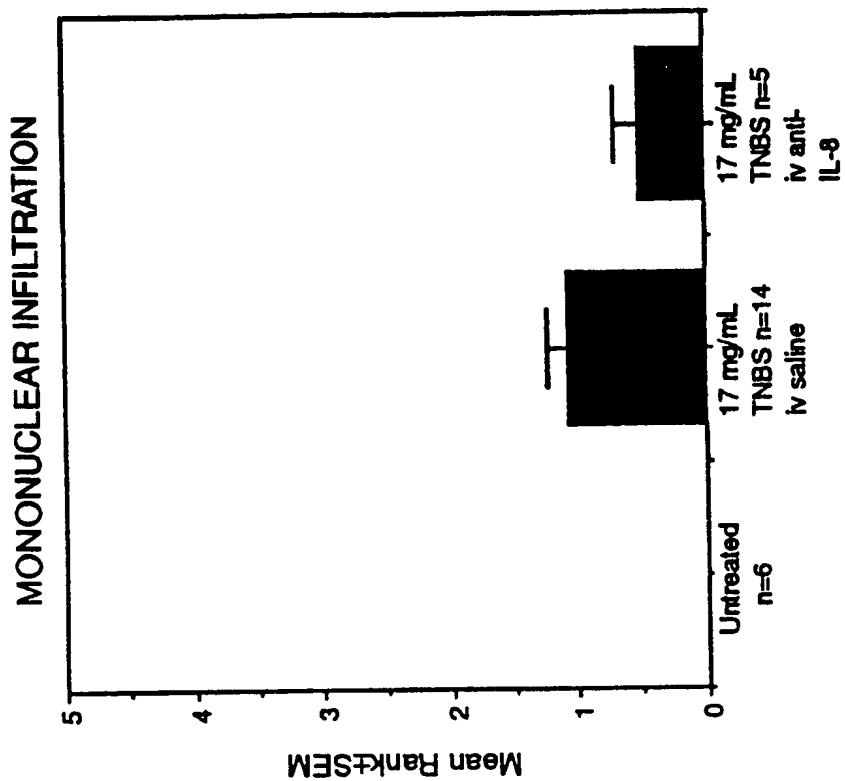


FIG. 11J

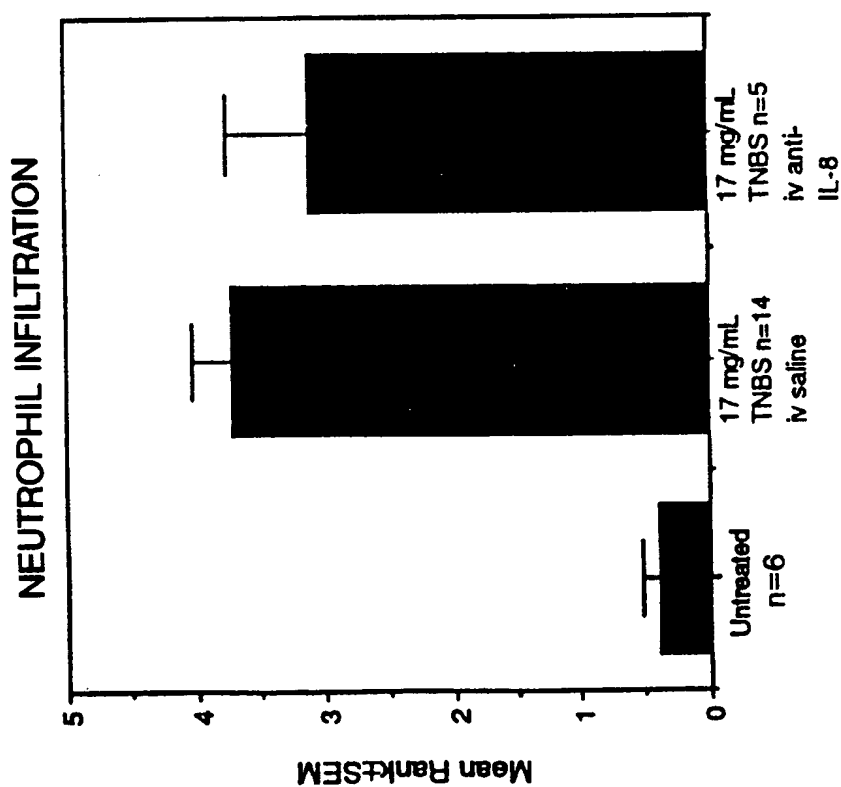
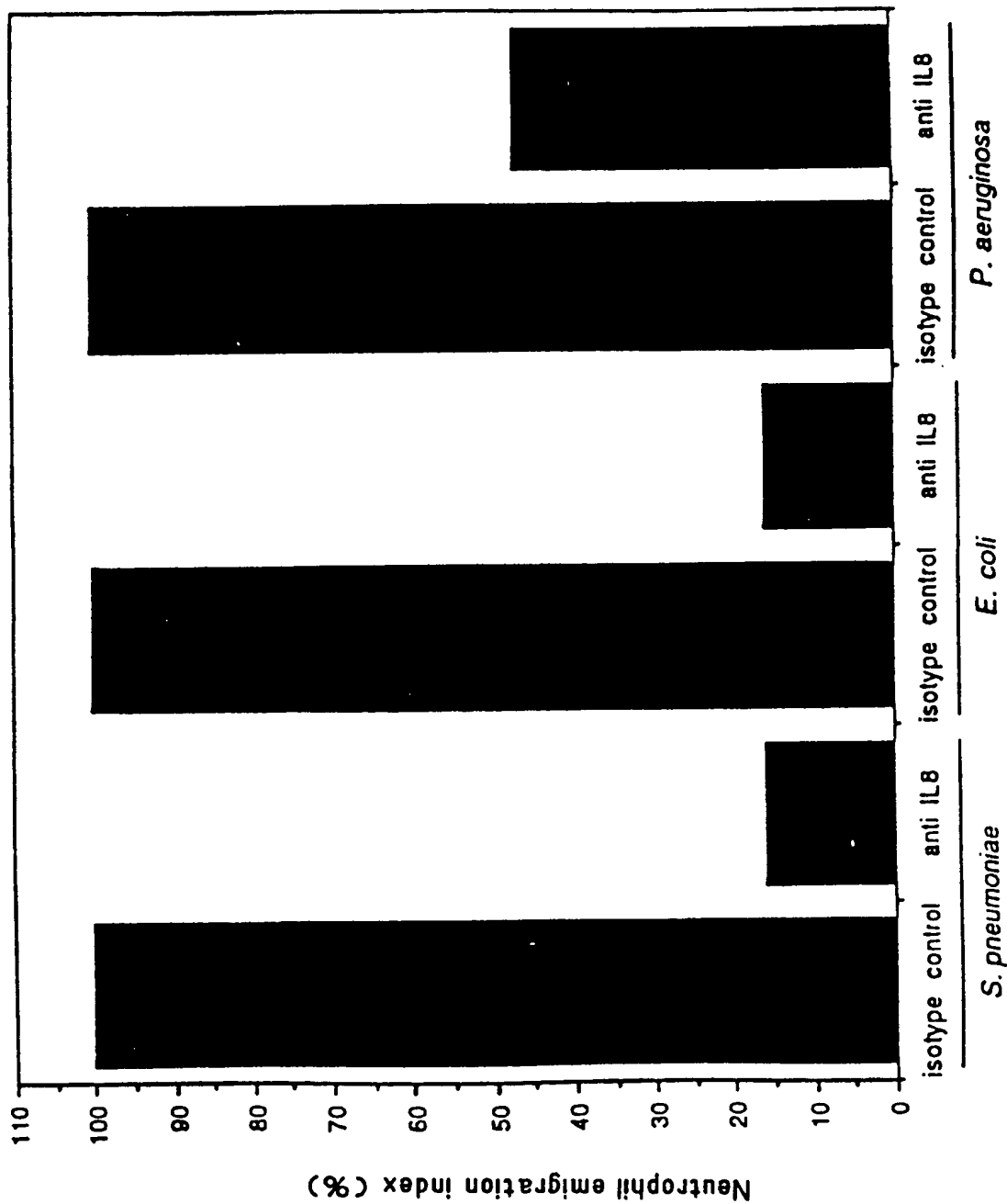


FIG. 11I

FIG. 12



Light Chain Primers:

FIG. 13

MKLC-1, 22mer

5' CAGTCCAACGTGTCAGGACGCC 3'

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3'

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3'

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3'

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3'

FIG. 14

Light chain forward primer

SL001A-2 35 mer

5' ACAAACGCGTACGCT GACATCGTCATGACCCAGTC 3'
 T T T
 A

Light chain reverse primer

SL001B 37 mer

5' GCTCTTCGAATG GTGGGAAGATGGATACAGTTGGTGC 3'

FIG. 15

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3'

T
G
A

C

SL002B 39-MER

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTTGGC 3'

T
A
G

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1 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC
CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCCAGTCG
1 D I V M T Q S Q K F M S T S V G D R V S

61 GTCACCTGCA AGGCCAGTCA GAATGTGGT ACTAATGTAG CCTGGTATCA ACAGAAACCA
CAGTGGACGT TCCGGTCAGT CTTACACCCA TGATTACATC GGACCATAGT TGTCTTTGGT
21 V T C K A S Q N V G T N V A W Y Q Q K P

CDR #1

121 GGGCAATCTC CTAAAGCACT GATTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT
CCC GTTAGAG GATTTCGTGA CTAAATGAGC AGTAGGATGG CCATGTCACC TCAGGGACTA
41 G Q S P K A L I Y S S Y R Y S G V P D

CDR #2

181 CGCTTCACAG GCAGTGGATC TGGACAGAT TTCACTCTCA CCATCAGCCA TGTGAGTCT
GCGAAGTGTG CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAAGTCGT ACACGTCAGA
61 R F T G S G S G T D F T L T I S H V Q S

241 GAAGACTTGG CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT
CTTCTGAACC GTCTGATAAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA
81 E D L A D Y F C Q Q Y N I Y P L T F G P

CDR #3

301 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC CATCTTCCA
CCCTGGTTCG ACCTCAACTT TGCCCCGACTA CGACGTGGTG GTTGACATAG GTAGAAGGT
101 G T K L E L K R A D A A P P T V S I F P

BstBI

361 CCATTTCGAA
GGTAAGCTT

121 P F E

FIG. 16

1 TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG GAGGCTTAGT
AAGATAACGA TGTTTTCGCA TCGCACTCCA CGTCGACCAC CTCAGACCCC CTCCGAATCA
1 E V Q L V E S G G G L V

61 GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT GGATTCATAT TCAGTAGTTA
CGGCGGACCT CCCAGGGACT TTGAGAGGAC ACGTCGGAGA CCTAAGTATA AGTCATCAAT
13 P P G G S L K L S C A A S G F I F S S Y
* *

CDR #1

121 TGGCATGTCT TGGGTTCGCC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTA
ACCGTACAGA ACCCAAGCGG TCTGAGGTCC GTTCTCGGAC CTCAACCAGC GTTGGTAATT
33 G M S W V R Q T P G K S L E L V A T I N
* * *

181 TAATAATGGT GATAGCACCT ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG
ATTATTACCA CTATCGTGGA TAATAGGTCT GTCACACTTC CCGGCTAAGT GGTAGAGGGC
53 N N G D S T Y Y P D S V K G R F T I S R
* * * * *

CDR #2

241 AGACAATGCC AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC
TCTGTACCG TTCTTGTGGG ACATGGACGT TTACTCGTCA GACTTCAGAC TCCTGTGTCG
73 D N A K N T L Y L Q M S S L K S E D T A

301 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT ACTGGGGCCA
GTACAAAATG ACACGTTCTC GGGAGTAATC AAGCCGATGA ACCAAACCAA TGACCCCGGT
93 M F Y C A R A L I S S A T W F G Y W G Q
* * * * *

CDR #3

361 AGGGACTCTG GTCAGTGTCT CTGCAGCCAA AACAAACAGCC CCATCTGTCT
TCCCTGAGAC CAGTGACAGA GACGTCGGTT TTGTTGTCGG GGTAACAGCA
113 G T L V T V S A A K T T A P S V Y

ApaI
411 ATCCGGG
TAGGCCC
130 P

FIG. 17

FIG. 18

VL.front 31-MER

5' ACAAACGCGTACGCTGATATCGTCCATGACAG 3'

VL.rear 31-MER

5' GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG 3'

VH.front.SPE 21-MER

5' CCACTAGTACGCAAGTTCAGG 3'

VH.rear 33-MER

5' GATGGGCCCTTGGTGGAGGCTGCAGAGACAGTG 3'

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1  ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT TGCTACAAAC
   TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61  GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA TGTCCACATC AGTAGGAGAC
   CGCATGCGAC TATAGCAGTA CTGTGTCAGA GTTTTTTAAGT ACAGGTGTAG TCATCCTCTG
-3  A Y A D I V M T Q S Q K F M S T S V G D

121 AGGGTCAGCG TCACCTGCAA GGCCAGTCAG AATGTGGGTA CTAATGTAGC CTGGTATCAA
   TCCCAGTCGC AGTGGACGTT CCGGTCAGTC TTACACCCAT GATTACATCG GACCATAGTT
18  R V S V T C K A S O N V G T N V A W Y Q
      * * * * * * * * * * * * * *
                                CDR #1

181 CAGAAACCAG GGCAATCTCC TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA
   GTCTTTGGTC CCGTTAGAGG ATTTCTGTGAC TAAATGAGCA GTAGGATGGC CATGTCACTT
38  Q K P G Q S P K A L I Y S S S Y R Y S G
      * * * * * * * * * *
                                CDR #2

241 GTCCCTGATC GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT
   CAGGGACTAG CGAAGTGTCC GTCACCTAGA CCCTGTCTAA AGTGAGAGTG GTAGTCGGTA
58  V P D R F T G S G S G T D F T L T I S H

301 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTCAGCAAT ATAACATCTA TCCTCTCACG
   CACGTCAGAC TTCTGAACCG TCTGATAAAG ACAGTCGTTA TATTGTAGAT AGGAGAGTGC
78  V Q S E D L A D Y F C Q Q Y N I Y P L T
      * * * * * * * * * *
                                CDR #3

                                BstBI
361 TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG CTGCACCATC TGTCTTCATC
   AAGCCAGGAC CCTGGTTCTGA CCTCGAAGCT TCTCGACACC GACGTGGTAG ACAGAAGTAG
98  F G P G T K L E L R R A V A A P S V F I

421 TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAAGTGTCT CTGTTGTGTG CCTGCTGAAT
   AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGAA GACAACACAC GGACGACTTA
118 F P P S D E Q L K S G T A S V V C L L N

481 AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT
   TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA
138 N F Y P R E A K V Q W K V D N A L Q S G

541 AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
   TTGAGGGTCC TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG
158 N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC
   TGGGACTGCG ACTCGTTTTC TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
178 T L T L S K A D Y E K H K V Y A C E V T

661 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG
   GTAGTCCCAG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC
198 H Q G L S S P V T K S F N R G E C

```

711 TTAA
AATT

216 O

FIG. 19

SUBSTITUTE SHEET (RULE 26)

6624405600

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N

61 GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT TAGTGCCGCC TGGAGGGTCC
 CGCATGCGAC TCCACGTCGA CCACCTCAGA CCCCTCCGA ATCACGGCGG ACCTCCCAGG
 -3 A Y A E V Q L V E S G G G L V P P G G S

121 CTGAAACTCT CCTGTGCAGC CTCTGGATTC ATATTCAGTA GTTATGGCAT GTCTTGGGTT
 GACTTTGAGA GGACACGTCG GAGACCTAAG TATAAGTCAT CAATACCGTA CAGAACCCAA
 18 L K L S C A A S G F I F S S Y G M S W V
 * * * *

CDR #1

181 CGCCAGACTC CAGGCAAGAG CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC
 GCGGTCTGAG GTCCGTTCTC GGACCTCAAC CAGCGTTGGT AATTATTATT ACCACTATCG
 38 R Q T P G K S L E L V A T I N N N G D S
 * * * *

241 ACCTATTATC CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC
 TGGATAATAG GTCTGTCACA CTTCCTGGCT AAGTGGTAGA GGGCTCTGTT ACGGTTCTTG
 58 T Y Y P D S V K G R F T I S R D N A K N
 * * * *

CDR #2

301 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT TTACTGTGCA
 TGGGACATGG ACGTTTACTC GTCAGACTTC AGACTCCTGT GTCGGTACAA AATGACACGT
 78 T L Y L Q M S S L K S E D T A M F Y C A

361 AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTACTGCGG GCCAAGGGAC TCTGGTCACT
 TCTCGGGAGT AATCAAGCCG ATGAACCAAA CCAATGACCC CGGTTCCCTG AGACCAGTGA
 98 R A L I S S A T W F G Y W G Q G T L V T
 * * * *

CDR #3

ApaI

421 GTCTCTGCAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCCCTC CTCCAAGAGC
 CAGAGACGTC GGAGGTGGTT CCCGGGTAGC CAGAAGGGGG ACCGTGGGAG GAGGTTCTCG
 118 V S A A S T K G P S V F P L A P S S K S

481 ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG
 TGGAGACCCC CGTGTGCGCCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC
 138 T S G G T A A L G C L V K D Y F P E P V

541 ACGGTGTCGT GGAACCTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA
 TGCCACAGCA CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT
 158 T V S W N S G A L T S G V H T F P A V L

601 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
 GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCACTGGC ACGGGAGGTC GTCGAACCCG
 178 Q S S G L Y S L S S V V T V P S S S L G

FIG. 20A

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661 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA
TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT
198 T Q T Y I C N V N H K P S N T K V D K K
721 GTTGAGCCCA AATCTTGTGA CAAAACACAC ACATGA
CAACTCGGGT TTAGAACACT GTTTGTAGTG TGTACT
218 V E P K S C D K T H T O

FIG. 20B

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Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAAC TGTTCAGGACGCC 3'

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3'

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3'

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3'

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3'

FIG. 21

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Light chain forward primer

6G4.light.Nsi 36-MER

5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC 3'
 T T T T
 A A

Light chain reverse primer

6G4.light.Mun 35-MER

5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3'

FIG. 22

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Heavy chain forward primer

6G4.heavy.Mlu 32-MER

5' CAAACGCGTACGCT GAG ATC CAG CTG CAG CAG 3'
 T C

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTGGC 3'
 T
 A
 G

FIG. 23

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70 G ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGAGAT
 C TATAGACTA CTGTGTCTGT GGTGAGAGG ACGGACAGTC AGAACCTCTA
 1 D I V M T Q T P L S L P V S L G D

121 CAGGCCTCCA TCTCTTGTCAG ATCTAGTCAG AGCCTTGTCAC ACGGTATTGG AAACACCTAT
 GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
 18 Q A S I S C R S S O S L V H G I G N T Y
 * * * * * * * * * * * * * *

CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
 AATGTAACCA TGGACGTCTT CCGTCCGGTC AGAGGTTTTCG AGGACTAGAT GTTTCAAAGG
 38 L H W Y L Q K P G Q S P K L L I Y K V S
 * * * * * * * * * *

CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTTACA
 TTGGCTAAAA GACCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
 58 N R F S G V P D R F S G S G S G T D F T
 * * * * *

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
 GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
 78 L R I S R V E A E D L G L Y F C S Q S T
 * * * * *

CDR #3

361 CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGATGCTGCA
 GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCCG ACTACGACGT
 98 H V P L T F G A G T K L E L K R A D A A
 * * * * *

MunI

421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA
 GGTGACATA GGTAGAAGGG TGGTAGGTCA CTCGTAACT
 118 P T V S I F P P S S E Q L K

FIG. 24

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70 G AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
 C TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
 1 E I Q L Q Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAGTA GCCACTACAT GCACTGGGTG
 CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
 18 V K I S C K A S G Y S F S S H Y M H W V
 * * * * *

CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
 TTCGTCTCGG TACCTTTCTC GGAAGTACC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K Q S H G K S L E W I G Y I D P S N G E
 * * * * *

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAGT GACATCTGTG TAGAAGGTCG
 58 T T Y N Q K F K G K A T L T V D T S S S
 * * * * *

301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
 TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
 78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
 TCTCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R G D Y R Y N G D W F F D V W G A G T T
 * * * * *

CDR #3

BstEII ApaI
 421 GTCACCGTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGCC
 CAGTGGCAGA GGAGGCGGAT TTGGCTGTCT GGGTAGCCAG ATAGGCCCGG
 118 V T V S S A K T D S P I G L S G P

471 CATC
 GTAG
 135 I

FIG. 25

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5' CTTGGTGGAGGCGGAGGAGACG 3'

Mutagenesis Primer for 6G425VL

DS/VF 38MER

5' GAAACGGGCTGTTGCTGCACCAACTGTATTCATCTTCC 3'

SYN.BstEII 31 MER

5' GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 3'

SYN.Apa 22 MER

5' CTTGGTGGAGGCGGAGGAGACG 3'

FIG. 26

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1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAT
TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA
-23 M K K N I A F L L A S M F V F S I A T N

61 GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
CGTATGCGAC TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
-3 A Y A D I V M T Q T P L S L P V S L G D

121 CAGGCCTCCA TCTCTTGCAAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT
GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
18 Q A S I S C R S S O S L V H G I G N T Y

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CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
AATGTAACCA TGGACGTCTT CGGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
38 L H W Y L Q K P G Q S P K L L I Y K V S

*

*

CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTTACA
TTGGCTAAAA GACCCCAAGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
58 N R F S G V P D R F S G S G S G T D F T
* * * *

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
78 L R I S R V E A E D L G L Y F C S Q S T

*

*

*

*

CDR #3

361 CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGTGCTGCA
GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCC ACAACGACGT
98 H V P L T F G A G T K L E L K R A V A A
* * * *

421 CCAACTGTAT TCATCTTCCC ACCATCCAGT GAGCAATTGA AATCTGGAAC TGCCTCTGTT
GGTTGACATA AGTAGAAGGG TGGTAGGTCA CTCGTTAAC TTAGACCTTG ACGGAGACAA
118 P T V F I F P P S S E Q L K S G T A S V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGA GGTGGATAAC
CACACGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V C L L N N F Y P R E A K V Q W K V D N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
CGGGAGGTTA GCCCATTGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

FIG. 27A

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661 GCCTGCCAAG TCACCCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
CGGACGCTTC AGTGGGTAGT CCCGGA CTG AGCGGCAGT GTTCTCGAA GTTGTCCTCCT
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTAA
CTCACAATT
218 E C O

FIG. 27B

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N

61 GCGTACGCTG AGATTTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
 CGCATGCGAC TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
 -3 A Y A E I Q L Q Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTTCAGTA GCCACTACAT GCACTGGGTG
 CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
 18 V K I S C K A S G Y S F S S H Y M H W V
 * * * * *

CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
 TTCGTCTCGG TACCTTTCTC GGAACCTACC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K Q S H G K S L E W I G Y I D P S N G E
 * * * * *

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAC TACATCTGTG TAGAAGGTCG
 58 T T Y N Q K F K G K A T L T V D T S S S
 * * * * *

301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
 TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
 78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
 TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R G D Y R Y N G D W F F D V W G A G T T
 * * * * *

CDR #3

421 GTCACCGTCT CCTCCGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
 CAGTGGCAGA GGAGGCGGAG GTGGTTCCCG GGTAGCCAGA AGGGGGACCG TGGGAGGAGG
 118 V T V S S A S T K G P S V F P L A P S S

481 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA
 TTCTCGTGGA GACCCCGGTG TCGCCGGGAC CCGACGGACC AGTTCCTGAT GAAGGGGCTT
 138 K S T S G G T A A L G C L V K D Y F P E

541 CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT
 GGCCACTGCC ACAGCACCTT GAGTCCGCGG GACTGGTCGC CGCACGTGTG GAAGGGCCGA
 158 P V T V S W N S G A L T S G V H T F P A

601 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC
 CAGGATGTCA GGAGTCCTGA GATGAGGGAG TCGTCGCACC ACTGGCACGG GAGGTCGTCG
 178 V L Q S S G L Y S L S S V V T V P S S S

FIG. 28A

SUBSTITUTE SHEET (RULE 26)

66EFG-4409E60

661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC
AACCCGTGGG TCTGGATGTA GACGTGTCAC TTAGTGTTCG GGTGTTGTG GTTCCACCTG
198 L G T Q T Y I C N V N H K P S N T K V D
721 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GA
TTCTTTCAAC TCGGGTTTAG AACACTGTTT TGAGTGTGTA CT
218 K K V E P K S C D K T H T O

FIG. 28B

```

10          20          abcde 30          40
6G425      DIVMTQTPLSLPVS LGDQASISCRSSQSLVHGIGNTYLHWY LQKPGQSPKLLIY
          #   #   #   #   #   #   #   #
F(ab)-1    DIQMTQSPSSLSASV GDRVTTITCRSSQSLVHGIGNTYLHWY QQKPGKAPKLLIY
          #   #   #   #   #   #   #   #
humkI      DIQMTQSPSSLSASV GDRVTTITCRASKTI-----SKYLAWYQQKPGKAPKLLIY
          #   #   #   #   #   #   #   #
          =====
          ++++++++
          L1

50          60          70          80          90          100
6G425      YKVS N R F S G V P D R F S D S G S G T D F T L R I S R V E A E D L G L Y F C S Q S T H V P L T F G A G T K L E L K R
          #   #   #   #   #   #   #   #
F(ab)-1    YKVS N R F S G V P S R F S G S G S G T D F T L T I S S L Q P E D F A T Y Y C S Q S T H V P L T F G Q G T K V E I K R
          #   #   #   #   #   #   #   #
humkI      Y S G S T L E S G V P S R F S G S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q H N E Y P L T F G Q G T K V E I K R
          #   #   #   #   #   #   #   #
          =====
          ++++++++
          L2          L3

```

```

10          20          30          40
6G425      EIQ LQQSGPELMKPGASVKISCKASGYFSSHYMHWVKQSHGKSLEWI
            #  ##  ##  ##  #  ###  #                #  ##  #  #
F(ab)-1    EVQLVESGGGLVQPGGSLRLSCAASGYFSSHYMHWVRQAPGKGLEWV
            #  ##  #  #
humIII     EVQLVESGGGLVQPGGSLRLSCAASGFSTGHWMNWVRQAPGKGLEWV
            =====
            ++++++
            H1

50  a          70          80  abc          90          100          110
6G425      GYIDPSNGETTYNQKFVKGKATLTVDTSSTANVHLSLTSDDSAVYFCAARGDYRYNGDWFFDVWGAGT
            ##  ##  #  ##  #####  ##  #  #                #
F(ab)-1    GYIDPSNGETTYNQKFGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAARGDYRYNGDWFFDVWGQGT
            #  #  ##  #  ##  ##  ##  ##  ##  ##  ##  ##  ##
humIII     GMIHPSDSETRYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAARGIYFY-GTTYFDYWGQGT
            =====
            ++++++
            H2
            H3

```

FIG. 29

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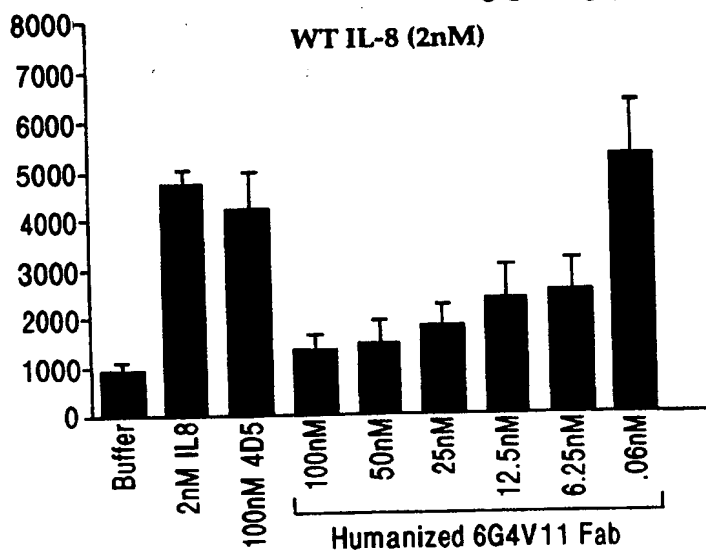


FIG. 30A

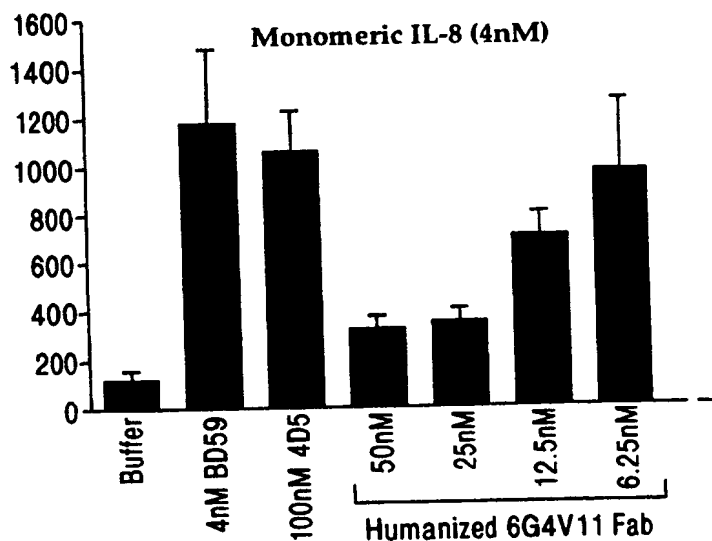
IC₅₀~12nM

FIG. 30B

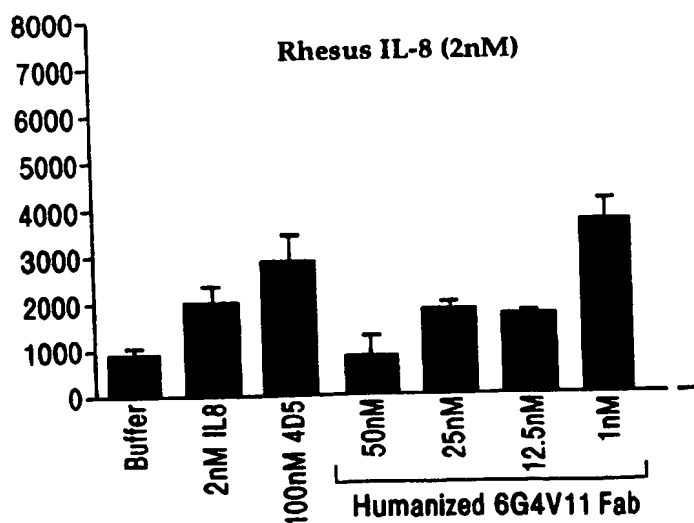
IC₅₀~15nM

FIG. 30C

IC₅₀~22nM

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTITCRSSQSLVHGIGNTY
LHWYQQKPKGAPKLLIYKVSNRFSGVPSRFSGSGTDFTLTISLQPEDFATYYCSQST
HVPLTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain

MKKNIAFLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT

Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)

SGGGSGSGDFDYKMANANKGAMTENADENALQSDAKGLDSVATDYGAIDFIGDVS
GLANGGATGDFAGSSNSQMAQVGDGDN SPLMNNFRQYLPQLPQSV ECRPFVFSAGKPY
EFSIDCDKINLFRGVFAFLLYVATFMYVFSTFANILRNKES

FIG. 31A

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A Y A D I Q M T Q S P S S L S A S V G D
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACACGTAT
 TCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
 18 R V T I T C R S S Q S L V H G I G N T Y
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
 AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L H W Y Q Q K P G K A P K L L I Y K V S
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N R F S G V P S R F S G S G S G T D F T
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L T I S S L Q P E D F A T Y Y C S Q S T
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H V P L T F G Q G T K V E I K R T V A A
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
 118 P S V F I F P P S D E Q L K S G T A S V
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
 138 V C L L N N F Y P R E A K V Q W K V D N
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 CGGGAGGTTA GCCATTGAG GGTCTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
 158 A L Q S G N S Q E S V T E Q D S K D S T
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
 178 Y S L S S T L T L S K A D Y E K H K V Y
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCTGAA GTTGTCCCTT
 198 A C E V T H Q G L S S P V T K S F N R G
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
 CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT
 218 E C O

FIG. 31B

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFTLTISSLPEDFATYYCSQST
HVP LTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSITYSLSSITLTLKADYEEKHKVYACEVTHQGLSSPVTKSFNRG
EC

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain

MKKNIAFLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVKQA PGKGLEWVG YIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT

FIG. 31C



FIG.32

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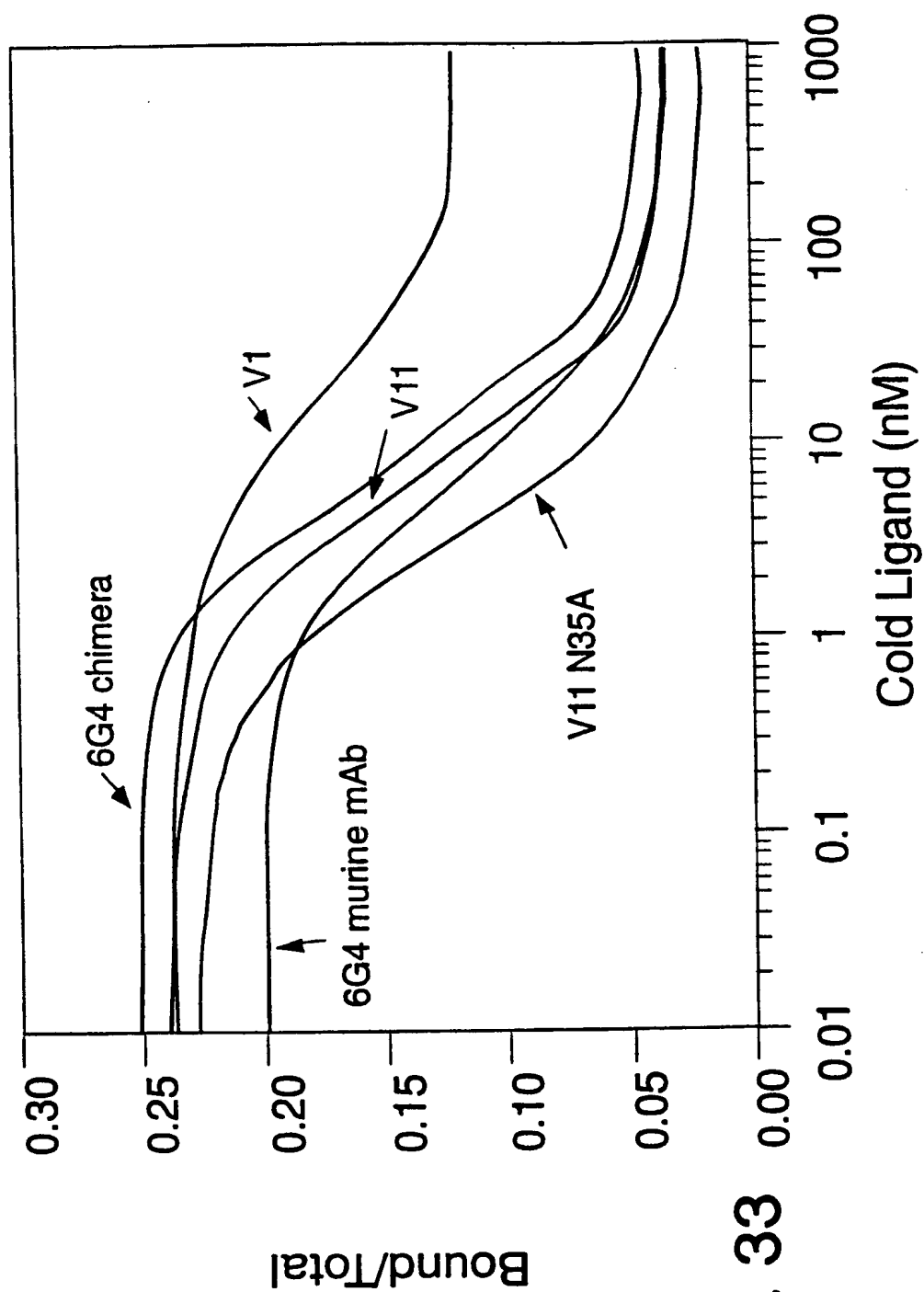
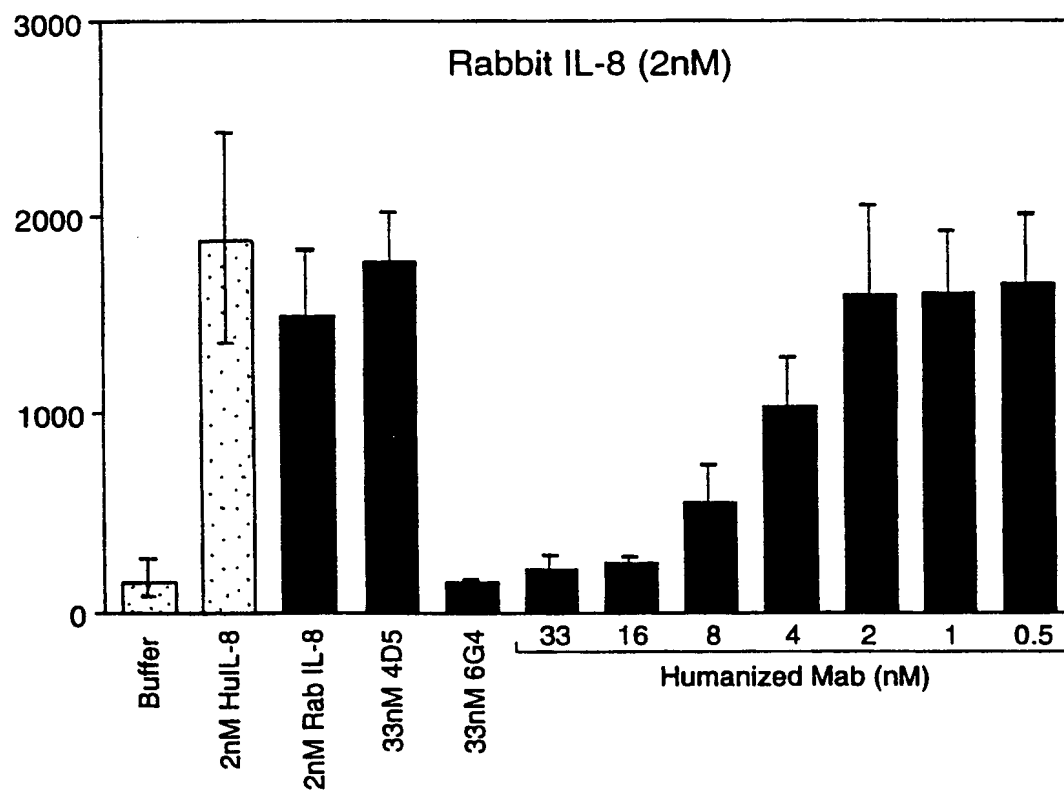
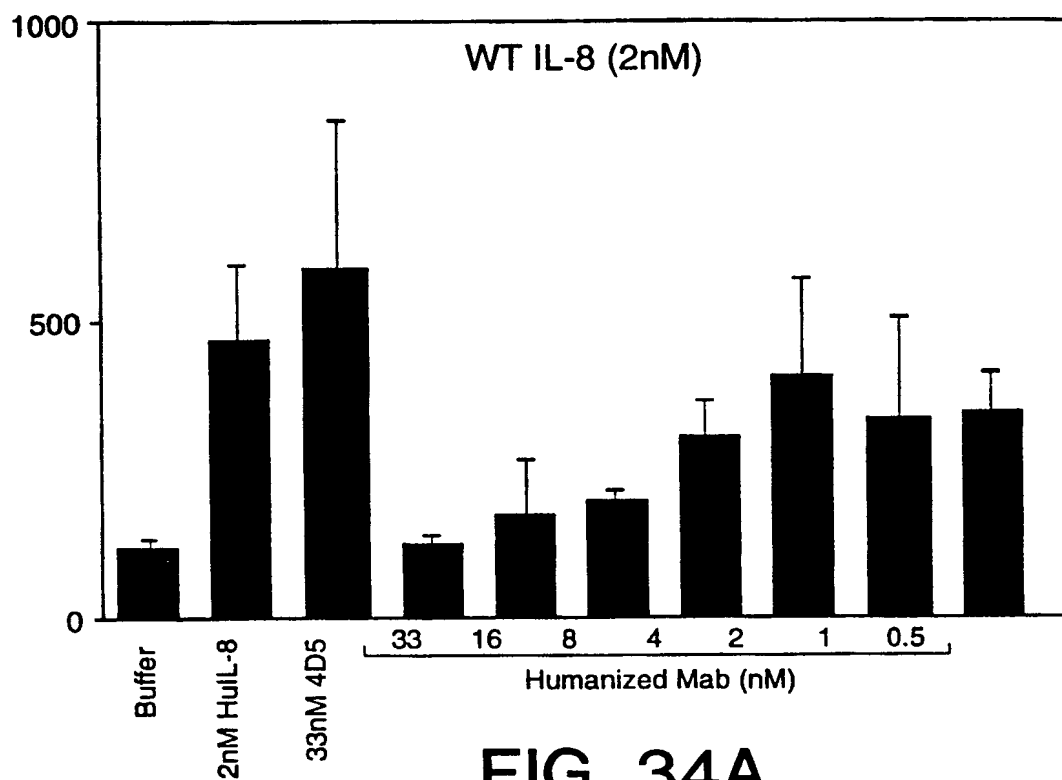


FIG. 33

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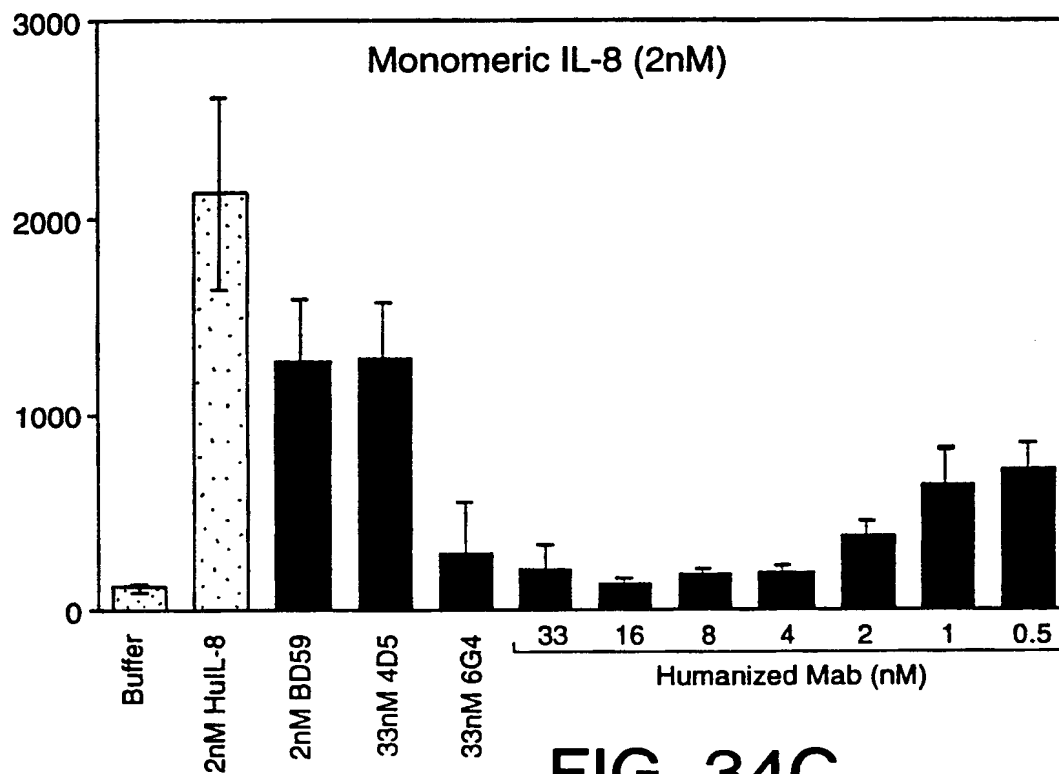


FIG. 34C

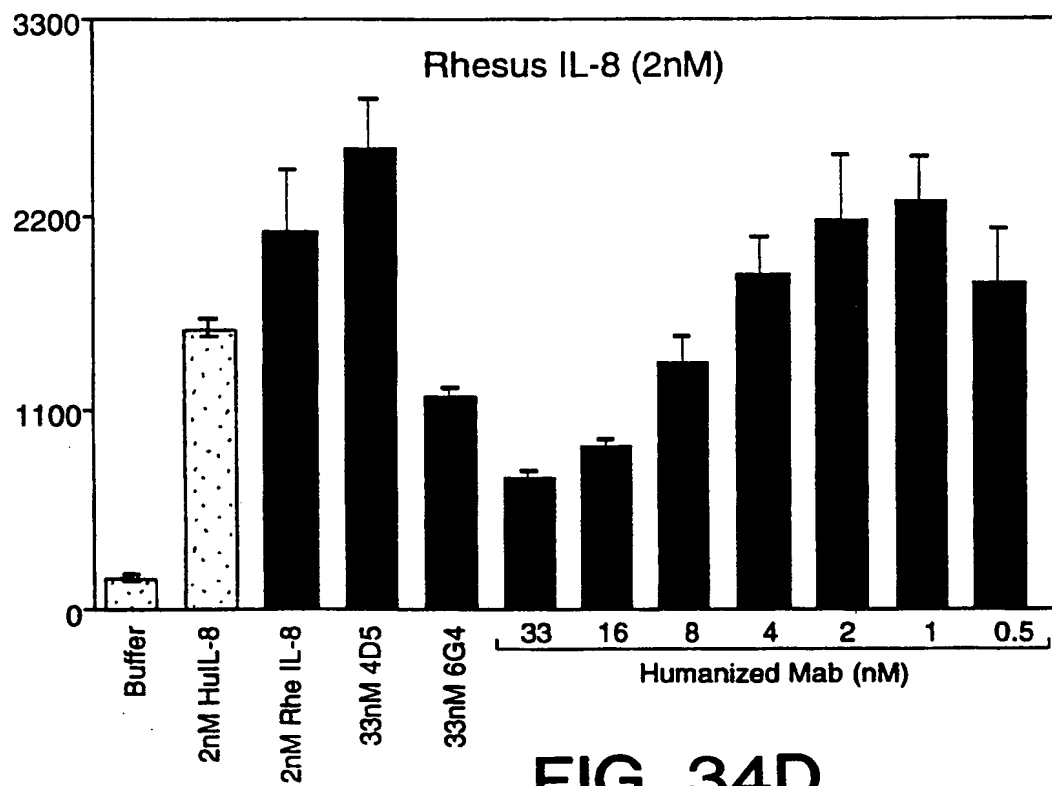


FIG. 34D

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Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTITCRSSQSLVHGIGATY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFTLTISLQPEDEATYYCSQST
HVPLTFGQGTEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain

MKKNIAFLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGVIDPSNGETTYNQFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT

Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper

CPPCPAPELLGGRMKQLEDKVEELLSKNYHLENEVARLKKLVGER

FIG. 35

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATAACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A Y A D I Q M T Q S P S S L S A S V G D
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
 18 R V T I T C R S S O S L V H G I G A T Y
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
 AATGTGACCA TAGTTGTCCT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L H W Y Q Q K P G K A P K L L I Y K V S
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N R F S G V P S R F S G S G S G T D F T
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L T I S S L Q P E D F A T Y Y C S Q S T
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H V P L T F G Q G T K V E I K R T V A A
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
 118 P S V F I F P P S D E Q L K S G T A S V
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
 138 V C L L N N F Y P R E A K V Q W K V D N
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 CGGGAGGTTA GCCCATGAG GGTCTCTCTCA CAGTGTCTCG TCCTGTCTGT CCTGTCTGTG
 158 A L Q S G N S Q E S V T E Q D S K D S T
 601 TACAGCCTCA GCAGCACCCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
 178 Y S L S S T L T L S K A D Y E K H K V Y
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 CGGACGCTTC AGTGGGTAGT CCCGGAAGTC AGCGGGCAGT GTTCTCTGAA GTTGTCCCTT
 198 A C E V T H Q G L S S P V T K S F N R G
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
 CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGACCCGG GATCATGCGT TGATCAGCAT
 218 E C O

FIG. 36

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781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
TTTTCCCATATA GATCTCCAAC TCCACTAAAA TACTTTTTTCT TATAGCGTAA AGAAGAACGT
-1 M K K N I A F L L A

841 TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCC CCGGTAAGGG CCTGGAATGG
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTTCC GGACCTTACC
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
CAACCTATAT AACTAGGAAG GTTACCACCT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCTAA TAGCGATGTT ACCACTGACC
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
TCGTGCGACC ACTGGCACGG GAGGTCGTG AACCCTGGG TCTGGATGTA GACGTTGCAC
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
TTAGTGTTTCG GGTCTGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA
TGAGTGTTGTA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTCGAT
228 T H T C P P C P A P E L L G G R M K Q L

FIG. 37A

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1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA
CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT
248 E D K V E E L L S K N Y H L E N E V A R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA
GAGTTTTTCG AACAGCCCCT CGCGATT
268 L K K L V G E R O

FIG. 37B

477,136

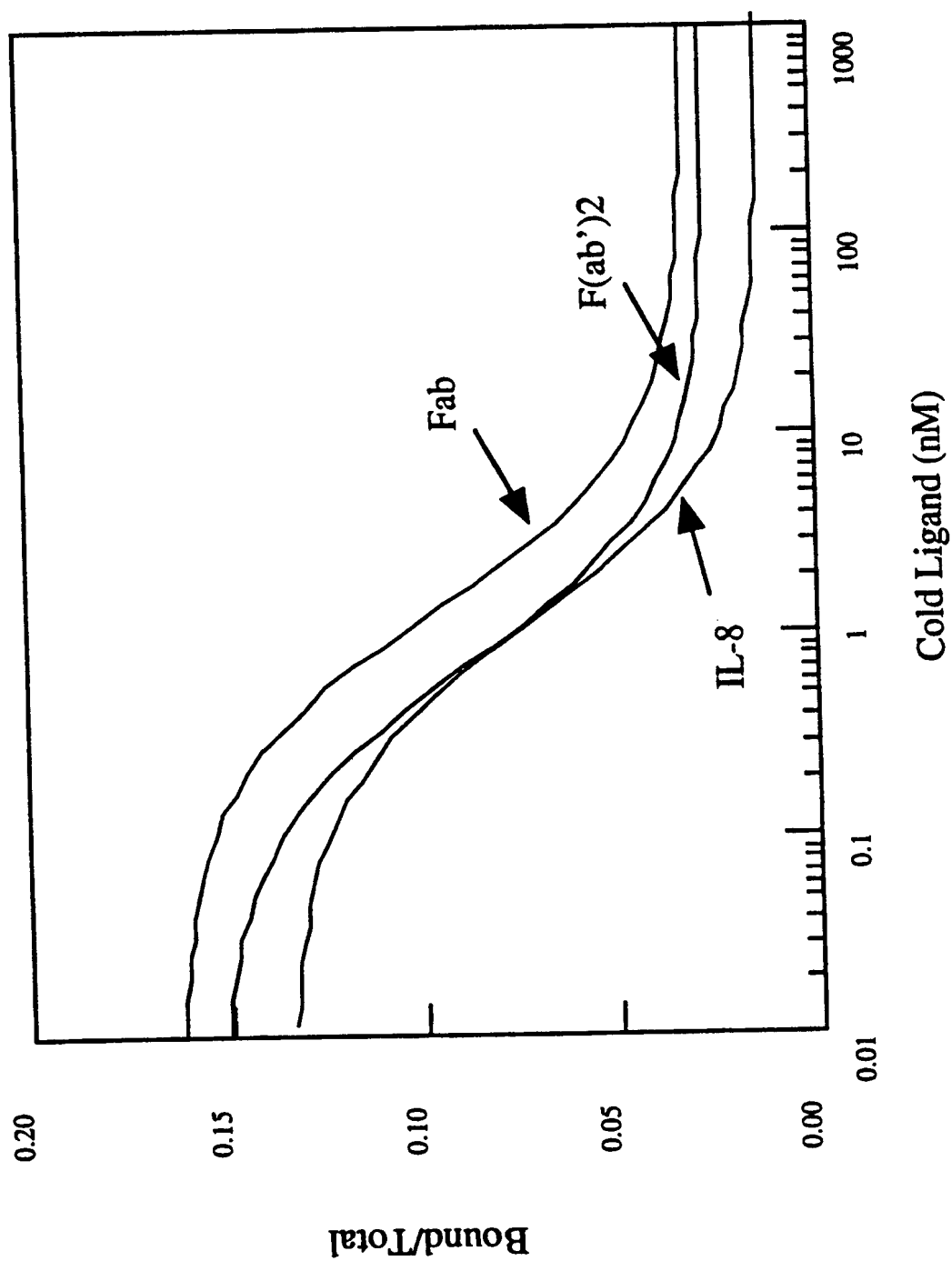


FIG. 38

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FIG. 39

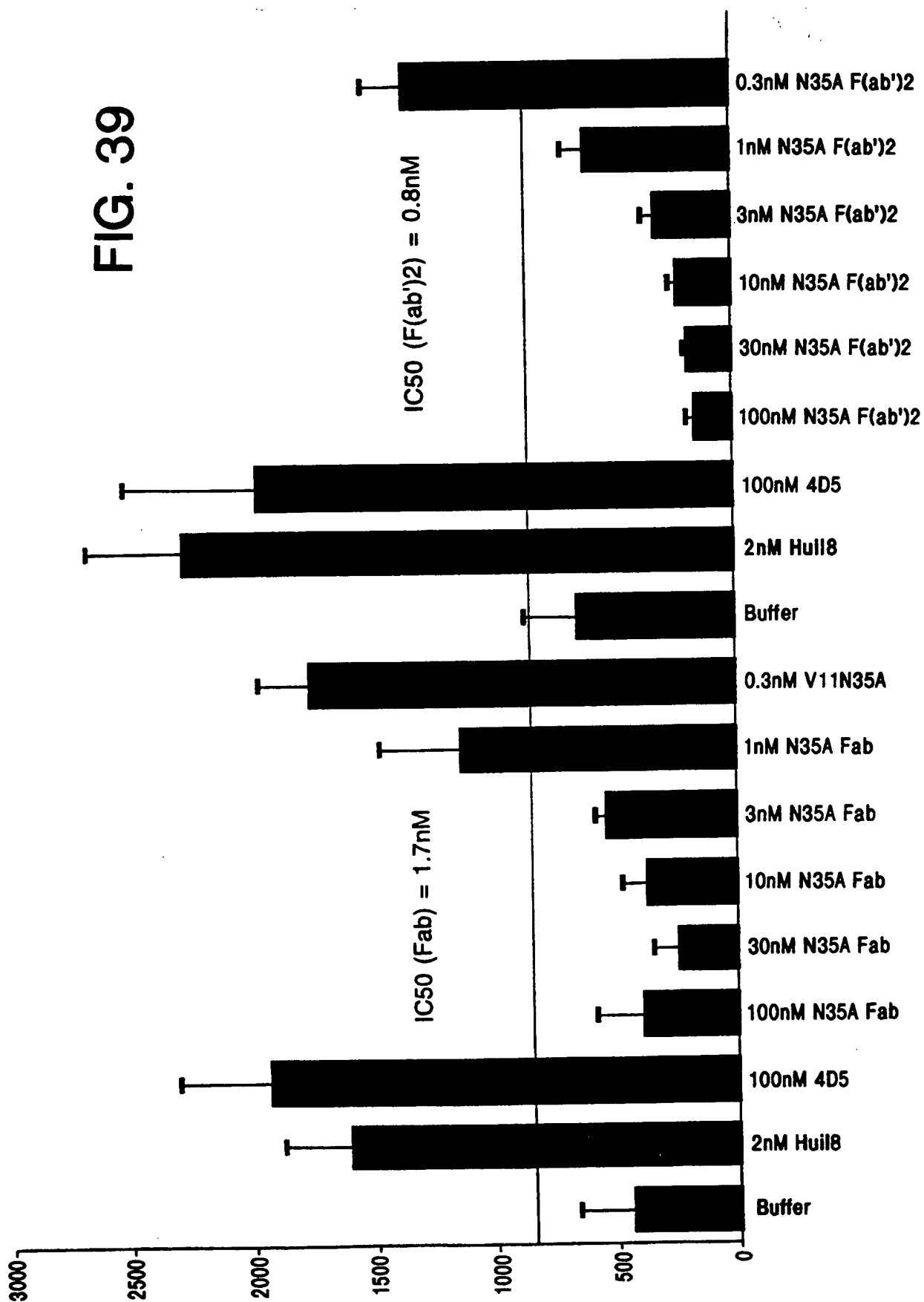


FIG. 40

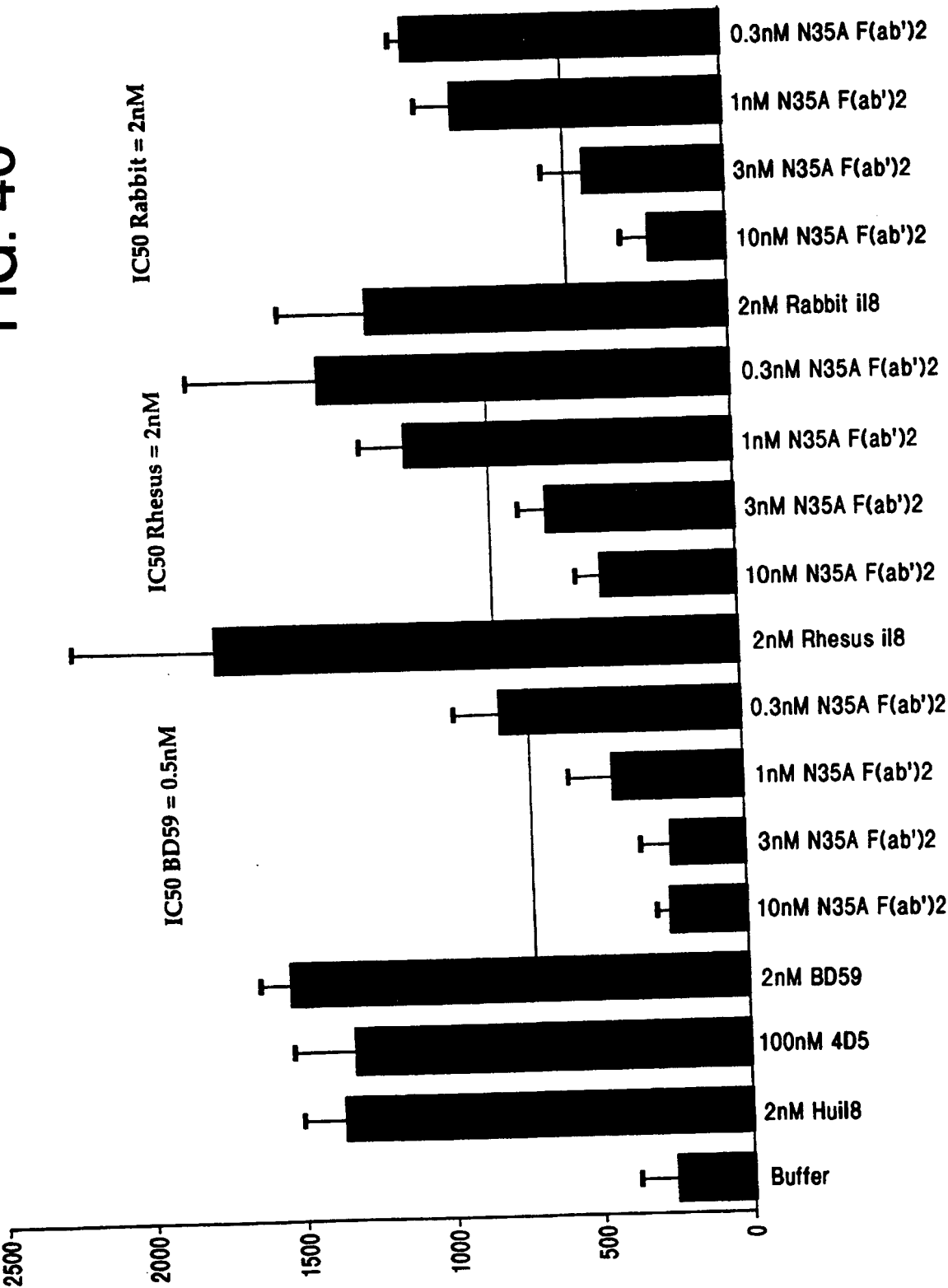


FIG. 41A

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scrFI
 nciI
 mspI
 hpaII
 dsav
 xmaI/pspAI
 smaI
 scrFI
 nciI
 dsav
 caulI
 bsaJI
 avai
 rsaI
 csp6I
 nlaIV
 kpnI
 hgiCI
 bani
 asp718
 acc65I
 401 TCGGTACCCG GGGATCCTCT CGAGGTGAG GTGATTTAT GAAAAGAAAT ATCGCATTTC TTCTTGCATC TATGTTTCGTT TTTTCTATTG CTACAACGC
 AGCCATGGGC CCTAGGAGA GTCCAACTC CACTAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC GATGTTGCG
 M K K N I A F L L A S M F V F S I A T N A
 a mutation was found that inactivated the mluI site. The penultimate nucleotide was changed fr G toT ^
 -23
 hphI
 mboII
 sfaNI
 mboII
 sfaNI
 sstI
 sacI
 hgiJII
 hgiAI/aspHI
 ecl136II
 bsp1286
 bsiHKAI
 bsmFI bmyI
 bsri
 tth111I/aspI
 ecorV
 501 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG TGGCGCATAG GGTACCATC ACCTGCAGGT CAAGTCAAG CTAGTACAT
 TAGCGGACTA TAGGTCTACT GGGTCAGGG CTGAGGGGAC AGCGGGAGAC ACCCGCTATC CCAGTGTAG TGGACGTCCA GTTCAGTTTC GAATCATGTA
 -2 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R S S Q S L V H
 hphI
 maeII
 bstEII
 hphI
 bspMI
 sse8387I
 pstI
 scfI
 bspMI
 ddeI
 nlaIII
 aluI
 rsaI
 hindIII
 csp6I

FIG. 41B

[illegible]

FIG. 41C

FIG. 41D

-23

1301 CTACAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCCTG GTGCGCCAG GGGGCTCACT CCGTTTCTCC TGTGCAGCTT CTGGCTACTC
GATGTTTCG CATGCGACTC CAAGTCGATC ACGTCAGACC GCCACCGGAC CACGTGCGTC CCCCGAGTGA GGCACACAGG ACACGTCGAA GACCGATGAG
-5 T N A Y A E V Q L V Q S G G G L V Q P G G S L R L S C A A S G Y S

scrFI
nciI
mspI
hpaII
dsav
cauII
bsII
xmaI/pspAI
smaI
scrFI
nciI
dsav
cauII
bsII

FIG. 41E

1401 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAAGGCC TGGATGGGT TGGATATATT GATCCTTCCA ATGCTGAAC TACGTATAAT
29 F S S H Y M H W V R Q A P G K G L E W V G Y I D P S N G E T T Y N
301 pleI
302 hinfi
303 taqi
304 xhoI
305 pae7I
306 aval
307 maeIII
308 sau96I
309 sau96I
310 sau96I
311 sau96I
312 sau96I
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701 sau96I

FIG. 41F

FIG. 41G

Patented

2001 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGGATGA AACAGCTAGA GGACAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA
AGTGTGTACG GCGGCACGG GTCGTGGTCT TGACACCCG CCGCCGTACT TTGTCGATCT CCTGTTCCAG CTTCTCGATG AGAGGTTCTT GATGGTGGAT
229 H T C P P C P A P E L L G G R M K Q L E D K V E E L L S K N Y H L
^junction between antibody and leucine zipper

2101 GAGAATGAAG TGGCAAGACT CAAAAGCTT GTCCGGGAGC GCTAAGCATG CGACGGCCCT AGAGTCCCTA ACCTCGGTT GCCGCCGGC GTTTTTTATT
CTCTTACTTC ACCGTTCTGA GTTTTTCGAA CAGCCCTTCG CGATTCTGATC GATTCGATC TCTCAGGGAT TCGAGGCCAA CGCGGCCCG CAAAAAATAA
262 E N E V A R L K K L V G E R O

2201 GTTAACTCAT GTTGACAGC TTATCATCGA TAAGCTTTAA TCGGGTAGTT TATCACAGTT AAATTGCTAA CGACTCAGG CACCGTGTAT GAAATCTAAC
CAATTGAGTA CAACTGTGC AATAGTAGCT ATTGGAATT ACGCCATCAA ATAGTGCTAA TTTAAGGATT CGTTCAGTCC GTGGCACATA CTTAGATTG

FIG. 41H

FIG. 41I

FIG. 41J

SUBSTITUTE SHEET (RULE 26)

fnu4HI
 bsoFI
 aciI
 thaI
 fnuDII/mvni
 bstUI
 cac8I
 sau3AI bshl236I
 mboI/ndeII[dam-]
 dpnII[dam+]
 dpnII[dam-]
 taqI[dam-]
 sau96I
 avaII
 bsrI
 sau3AI
 sau3AI asuI
 mboI/ndeII[dam-]
 mboI/ndeII[dam-]
 dpnI[dam+] nspBII
 dpnII[dam-]
 aciI
 maeIII
 dpnI[dam+]
 dpnII[dam-]
 aciI dpnII[dam-]
 CGATCACTGG ACCGCTGATC GTCACGGCGA
 TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTGGCATG
 GAGCCGCTCG TGTACCTTGC CCAACCGTAC
 TCGGATTGAA GCTAGTGACC TGGCGACTAG CAGTGCCGCT
 AGCCTAACIT AGCCTTAACC GGCTCTTACC
 GATCGCTCG GGCTCTTACC
 CCGAGAAATGG CTAGCGAGCG

fnu4HI
 bsoFI
 hinPI
 hhai/cfoI
 nlaIV
 nari
 kasi
 hinII/acyI
 hgiCI
 haeII
 bani aciI
 ahaII/bsaHI
 340I GATTGTAGGC GCCGCCCTAT ACCTTGCTCTG CCTCCCCGCG TTGCGTCCG GTGCATGGAG CCGGGCCACC TCGACCTGAA TGAAGCCG CGGCACCTCG
 CTAACATCCG CGCGGGGATA TGAACAGAC GGAGGGGCGC AACGCAGCGC CACGTACCTC GGCCCCGTGG AGCTGGACTT ACCTTCGGCC GCCGTGGAGC
 haeIII/pali
 sau96I
 scrFI
 ncil
 mspi
 hpaII
 dsav
 nlaIV asuI taqI
 cauII mnlI
 hgaI aciI nlaIII
 bstUI bstUI
 bshI236I bshI236I
 aciI hgaI
 fnuDII/mvni
 fnuDII/mvni
 thaI fnuDII/mvni
 thaI
 fnu4HI
 bsoFI
 aciI
 mspi
 hpaII
 nlaIV
 hgiCI
 cfrI0I/bsrFI
 cac8I bani
 CGGCACCTCG

FIG. 41L

3501 CTAACGGATT CACCACCTCCA AGAATTGGAG CCAATCAATT CTTGGGGAGA ACTGTGAATG CGCAAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC
GATTGCCATA GTGGTGAGGT TCTTAACCTC GGTAGTTAA GAACGCCCTCT TGACACTTAC CGTTTGGTT GGAACCCGTC TTGTATAGGT AGCGCAGGCG

3601 CATCTCCAGC AGCGGCACGC GCGGCATCTC GGGCAGCGTT GGGTCTGGC CACGGGTGGC GTACTAGCAC GAGGACAGCA ACTCCTGGGC CGATCCGACC
GTAGAGTGC TCGCGGTGC CGCGTAGAG CCCGTGCAA

FIG. 41M

sau3AI
mboI/ndeII[dam-]
mami[dam-]
dpuI[dam+]
dpuII[dam-]
bstYI/xhoII
alwI[dam-]
mspi
hpaiI
mroI bsaBI[dam-]
bspMI
bspEI[dam-]
bsaWI sfaNI
accIII[dam-]
fnu4HI
bsoFI
bbvI
sfaNI
foki
cac8I
TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC
AATACAAGGC CTAGACGTAG CGTCCTACGA CGACCGATGG

3801 TGGTCTTCGG TTTCCGGTGT TCGTAAAGTC TGAAGTCAGG CCCTGCACCA
ACCAAGGCC AAGGCACAA AGCATTTTCAG ACCTTTGGCG CTTCACTCGC GGGACGTGGT

acII
thai
fnuDII/mvni hinPI
bstUI hhaI/cfoI
bsh1236I haeII
mslI
TGAAGTCGAG CCCTGCACCA
CTTCAGTCGC ACTGGGACTC ACTAAAGA
TGACCCCTGAG TGATTTTCT
CTGGTCCGC CGCATCCATA
CGCCAGTTG TTTACCCCTCA
GCGGAGTAT GCGGTCTAAC
AAATGGGAGT

3901 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT
GACACCTTGT GGATGTAGAC ATAATTGCTT CCGCACCGTA
ACTGGGACTC ACTAAAGA

cac8I
hinPI
hhaI/cfoI
tru9I haeII
mseI eco47III
dcl
asul bsoFI
bsrI
acII
mnlI

4001 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT
GACACCTTGT GGATGTAGAC ATAATTGCTT CCGCACCGTA
ACTGGGACTC ACTAAAGA
GTATCGTGAG CATCCTCTCT
CGTTTCATCG GTATCATTCAC
CCCCATGAAC AGAAATTCCTC
GGGTACTTG TCTTAAGGG

nsPI
scrFI
ncII
mspi
bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG

bsrI
bsII
maeII
psp1406I
CAACGTTCCA
GTTGCAAGGT
maeII
maeIII
nspHI
GTAACGGGC
ATGTTTCATCA
TCAAGTAGT
AGTCATTGGG
CATAGCACTC
GTAGGAGAGA
GCAAAGTAGC
CATAGTAATG
GGGTACTTG
TCTTAAGGG
</

FIG. 41N

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cac8I
 sau96I
 tru9I haeIII/palI
 mseI
 aciI bslI nlaIII aciI
 asuI
 bpmI/gsuI[dcM-]
 4101 CCTTACACGG AGGCATCAAG TGACCAACA GGAACCAACC GCCCTTAACA TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAACTCAAC
 GGAATGTGCC TCCGTAGTTC ACTGCTTGT CTTTTTTGG CGGGAATTGT ACCGGCGAA ATAGTCTTCG GTCTGTAATT GCGAAGACCT CTTTGAGTTG
 fnu4HI thai
 bsoFI fnuDII/mvni
 aluI bstOI
 pvuII hinPI
 nspBII hhaI/cfoI
 fnu4HI thai
 bsoFI fnuDII/mvni
 bcgI bstOI
 bbvI mnlI bsh1236I
 4201 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTACGACCA CGCTGATGAG CTTTACGCA GCTGCCCTGC GCGTTTCGGT GATGACGGTG
 CTCGACCTGC GCCTACTTGT CCGTCTGTAG AACTTAGCG AAGTGCTGGT GCGACTACTC GAATGGCGT CGACGGAGCG CGCAAGCCA CTACTGCCAC
 aluI hgaI foki
 asp700
 xmnI
 tfiI
 hinfi
 mnlI
 aluI
 aciI
 nciI
 mspI
 hpaII
 sfaNI
 foki dsav
 aciI cauII
 drdI
 4301 AAAACCTCTG ACACATGCAG CTCGCGGAGA CGGTACAGC TTGTCTGTAA GCGGATGCCG GGAGCAGACA AGCCGCTCAG GCGCGTCAG CGGGTGTGG
 TTTTGAGAC TGTGTACGTC GAGGGCTCT GCGAGTGTG CCAAGATTC GCGTACGGC CCTGCTGT TCGGCGAGTC CGCGGAGTC GCCACACACC
 hgaI
 thai
 fnuDII/mvni
 bstOI aciI
 bsh1236I
 hinPI nspBII
 hhaI/cfoI
 aciI

FIG. 410

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4401 CGGGTGTGGG GCGGACGCA TGACCCAGTC ACCTAGCGAT AGCGAGTGT ATACTGGTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC
 GCCCACAGCC CCGGTGGT ACTGGGTGAG TGCATCGCTA TCGCCTCACA TATGACCGAA TTGATACGCC GTAGTCTCGT CTAACTATGAC TCTCAGCTGG
 fnu4HI bsoFI bsvI maeII maeII maeII
 hinPI nlaIII bsrI bsaI
 hhaI/cfoI tth111I/aspI
 4501 ATATCGGTG TGAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC AGCGCTCTT CCGCTTCTC GCTCACTGAC TCGCTGGCT CGTCTGTCG
 TATAGGCCAC ACTTATGGC GTGTCTACGC ATTCTCTTT TATGGCGTAG TCCGCGAGAA GCGAAGGAG CGAGTACTG AGCGACGCGA GCCAGCAAGC
 acII acII acII sfanI sfanI
 fnu4HI bsoFI bsvI maeII maeII maeII
 hinPI nlaIII bsrI bsaI
 hhaI/cfoI tth111I/aspI
 4601 GCTGCGCGA GCGGTATCAG CTCACCTCAA GCGGTAATA CCGTTATCCA CAGATCAGG GGATAACGCA GGAAAGACA GTGAGCAGAA AGGCCAGCAA
 CGACGCGCT CGCCATAGTC GAGTGAGTTT CGCCATTAT GCCAATAGGT GTCTTAGTCC CCTATTGGT CCTTTCTGT ACACCTGTTT TCCGGTCTGT
 fnu4HI bsoFI acII acII acII
 fnu4HI bsoFI bsvI maeII maeII maeII
 hinPI nlaIII bsrI bsaI
 hhaI/cfoI tth111I/aspI
 4701 AAGGCCAGG ACCGTAAAA GCGCGCTTG CTGGCGTTTT TCCATAGCT CCGCCCCCT GACGAGCATC AAAAAATCG ACGTCAAGT CAGAGGTGGC
 TTCCGGTCTT TGGCATTTTT CCGGCGCAAC GACCGCAAA AGGTATCCGA GCGGGGGGA CTGCTCGTAG TGTCTTTAGC TCGAGTTCA GTCTCCACCG
 scrFI mvaI ecorII dsav bstNI bslI apyI[dcM+] haeIII/palI haeI nlaIV
 fnu4HI bsoFI bsvI maeII maeII maeII
 hinPI nlaIII bsrI bsaI
 hhaI/cfoI tth111I/aspI
 4801 AAGGCCAGG ACCGTAAAA GCGCGCTTG CTGGCGTTTT TCCATAGCT CCGCCCCCT GACGAGCATC AAAAAATCG ACGTCAAGT CAGAGGTGGC
 TTCCGGTCTT TGGCATTTTT CCGGCGCAAC GACCGCAAA AGGTATCCGA GCGGGGGGA CTGCTCGTAG TGTCTTTAGC TCGAGTTCA GTCTCCACCG
 fnu4HI bsoFI bsvI maeII maeII maeII
 hinPI nlaIII bsrI bsaI
 hhaI/cfoI tth111I/aspI

FIG. 41P

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4801 GAAACCCGAC AGGACTATAA AGTACCAGG CGTTTCCCC TGAAGCTCC CTCGTGGCT CTCCTGTTCC GACCTGCCC CTTACCGGAT ACCTGTCCGC
 CTTTGGGCTG TCCTGATATT TCTATGCTCC GCAAGGGGG ACCTTCGAGG GAGCAGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA TGGACAGGCG

4901 CTTTCTCCCT TCGGAAGCG TGGCGCTTC TCATAGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGGTCCA AGCTGGGCTG TGTGCACGAA
 GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC ACACGTGCTT

5001 CCCCCGTTTC AGCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACAGG ACTTATCGCC ACTGGCAGCA GCCACTGGTA
 GGGGGGCAAG TCGGGCTGCG GACGCGGAAT AGGCCATTGA TAGCAGAACT CAGGTGGGC CATTCCTGTC TGAATAGCGG TGACCGTCTG CCGTGACCAT

5101 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTG GTATCTGCGC
 TGTCCTAATC GTCTCGCTCC ATACATCCGC CAGGATGCT CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCC TGTCATNAAC CATAGACGCG

Restriction enzymes and sites indicated in the sequence:

- scrFI mvaI mvaI ecorII dsav bstNI bstNI apyI[dcM+] bsajI aluI mnlI hhaI/cfoI hinPI bssSI bslI
- scrFI mspI fnu4HI hpaII bsoFI bsaWI aciI
- hgiAI/aspHI bspI286 bsiHKAI bmyI apaLI/snoI alw44I/snoI
- alwNI[dcM-] fnu4HI bsoFI fnu4HI bsoFI bbvI bsrI bbvI bsrI
- hinPI hhaI/cfoI haeII aluI aluI scfI ddel
- fnu4HI bsoFI nsp8II aciI hinPI maeIII mspI bsaWI mcrI bbvI bsrI hhaI/cfoI hpaII
- pleI hinPI cauII dsav nciI scrFI hpaII mspI
- bslI imai maeI bfaI haeIII/palI haeI
- mnlI aciI scfI

FIG. 41Q

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```

        mspI
        hpaII
        sau3AI
        mboI/ndeII[dam-]
        dpnI[dam+]
        dpnII[dam-]
        alwI[dam-]
        nspBII
        aciI
        cac8I
        fnu4HI
        bsoFI
        bbvI
        eco57I bsrI
        maeIII
        5201 TCTGCTGAAG CCAGTTACCT TCGAAAAAAG AGTTGGTAGC TCTTGATCCG GCAACAACAC CACCGCTGGT AGCGGTGGTT TTTTGGTTTG CAAGCAGCAG
        AGAGGACTTC GGTCAATGGA AGCCTTTTTC TCAACCATCG AGAAGTAGGC CGTTTGGTTG GTGGCGACCA TCGCCACCAA AAAACAAC GTTCTGTCGTC

        hinPI
        hhaI/cfoI
        thaI
        fnuDII/mvni
        bstUI
        bsh1236I
        5301 ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG ATTTTGGTCA
        TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT AGAAAGATG CCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC TAAACCCAGT

        sau3AI
        mboI/ndeII[dam-]
        mboI/ndeII[dam-]
        sau3AI
        mboI/ndeII[dam-]
        dpnI[dam+]
        dpnII[dam-]
        dpnI[dam+]
        dpnII[dam-]
        bstYI/xhoII
        alwI[dam-]
        bstYI/xhoII
        alwI[dam-]
        bstYI/xhoII
        alwI[dam-]
        hgaI ddeI
        tru9I
        mseI
        maeII
        nlaIII
        rcaI
        bspHI
        sau3AI
        mboI/ndeII[dam-]
        mboI/ndeII[dam-]
        hphI
        dpnI[dam+]
        mboII[dam-]
        sau3AI
        maeI
        tru9I
        mseI
        mboI/ndeII[dam-]
        dpnI[dam+]
        dpnII[dam-]
        dpnII[dam-]
        alwI[dam-]
        tru9I
        mseI
        bstYI/xhoII
        bstYI/xhoII
        alwI[dam-]
        bfaI
        ahaIII/draI
        ahaIII/draI
        5401 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA AGTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA
        ACTCTAATAG TTTTTCCTAG AAGTGGATCT AGGAAATTT AATTTTACT TCMAAATTTA GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT

        nlaIV
        hgiCI
        bani
        mnlI
        5501 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTTCGTT CATCCAVAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG
        GGTACGAAT TAGTCACCTCC GTGGATAGAG TCGCTAGACA GATAAGCAA GTAGGTATCA ACGGACTGAG GGCAGCACA TCTATTGATG CTATGCCCTC

        pleI
        hinfi
        ahdI/eam1105I
        foki
        sau3AI
        mboI/ndeII[dam-]
        dpnI[dam+]
        dpnII[dam-]
        ddeI
        mnlI
        mseI
        tru9I
        mnlI

```

FIG. 41R

[illegible]

FIG. 41S

FIG. 41T

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6401 TCGTCTCATG AGCGGATACA TATTGATG TATTAGAA AATAACAA TAGGGTTCC GCGACATT CCCCAGAAAG TGCCACCTGA CGTCTAAGAA
 AACAGAGTAC TCGCCTATGT ATAACTTAC ATAACTCTT TTATTGTTT ATCCCAAGG CGCGTGTAA GGGGCTTTC ACGGTGGACT GCAGATTCTT
 nlaIII rcaI bspHI acII nlaIV hhaI/cfoI
 bsmAI bsrBI
 hinPI
 thal
 fnuDII/mvnI
 bstUI
 bsh1236I
 aciI
 maeII
 hinII/acyI
 ahaII/bsaHI
 aatII ddeI
 sau96I
 haeIII/palI
 asuI
 mboII
 ecoO109I/draII
 mnlI
 bpuAI
 bbsI
 nlaIII rcaI tru9I
 bspHI mseI
 6501 ACCATTATTA TCATGACATT AACCTATATA AATAGGCGTA TCACGAGGCC CTTTCGTCTT CAA
 TGGTAATAAT AGTACTGTAA TTGGATATTT TTATCCGCAT AGTCTCCGG GAAAGCAGAA GTT

FIG. 41U

```

>length: 6563

aatII(GACGTC):      1645 6489
acc65I(GGTACC):      403 823
acci(GTMKAC):        1093 1963 4449
accII(TCCGGA):      3867[dam-]
aciI(CCGC):          178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
                    2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
                    3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
                    4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
                    5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
acyI
see hinI
aflIII(ACRYGT):      1307 4678
ageI(ACCGGT):        1788
ahaII/bsaHI(GRCGYC): 1645 1813 2616 2637 2751 3408 6107 6489
ahaIII/draI(TTTAAA): 5435 5454 6146
ahdI/eam1105I(GACNNNNNGTC): 346 5566
alulI(AGCT):         72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
                    2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
                    5922
alw44I/snoI(GTGCAC): 1831 4494 4992 6238
alwI[dam-](GGATC):   412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
                    6196 6214
alwNI[dcn-](CAGNNNCTG): 1117 1385 5089
apaI(GGGCCC):        1695
apaLI/snoI(GTGCAC):  1831 4494 4992 6238
apoI(RAATTY):         1 391 4093
apyI[dcn+](CCWGG):   640 999 1347 1357 1449 1665 1713 1755 1764 2333 3262 3645 4705 4826 4839
aseI/asnI/vsPI(ATTAAAT): 5742
asnI
see aseI
asp700(GAANNNTTC):   905 930 4234 6166
asp718(GGTACC):      403 823
aspHI
see hgiAI
see tth111I
asulI(GGNCC):        1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463

```

FIG. 41V

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Stop Template Primer

SL.97.2 5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3'

NNS Randomization Primer

SL.97.3 5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3'

FIG. 42

Randomization of Position N35 of Variable Light Chain CDR-1
Amino Acid Frequency

Phage Display (NNS Codon Library) Sort #3

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

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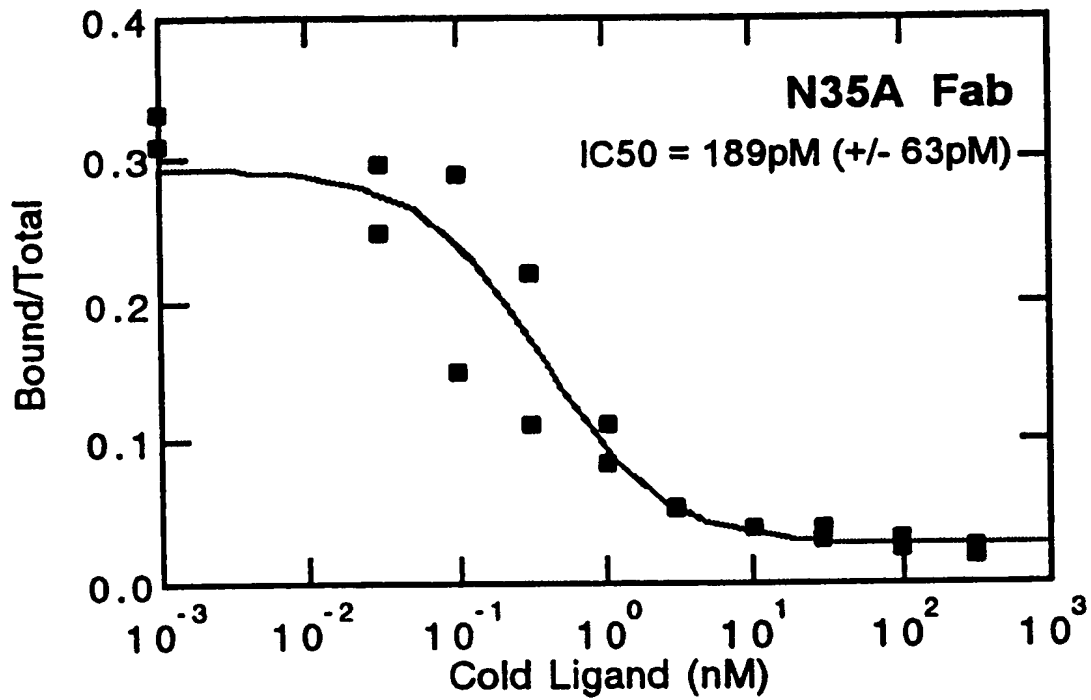


FIG. 43B-1

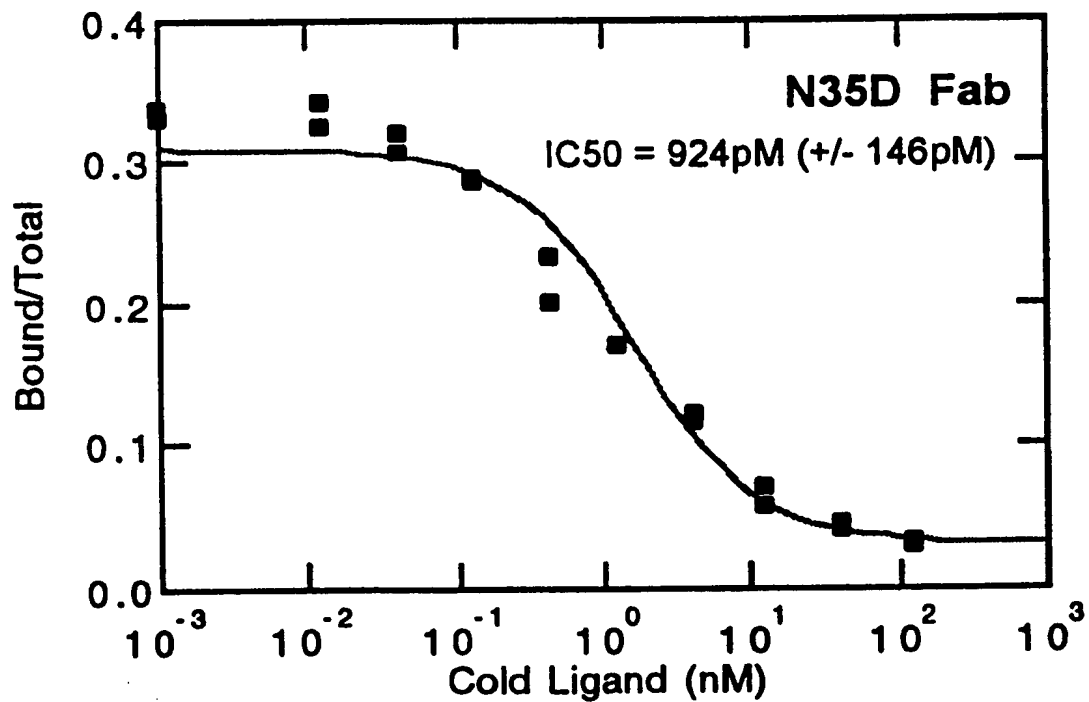


FIG. 43B-2

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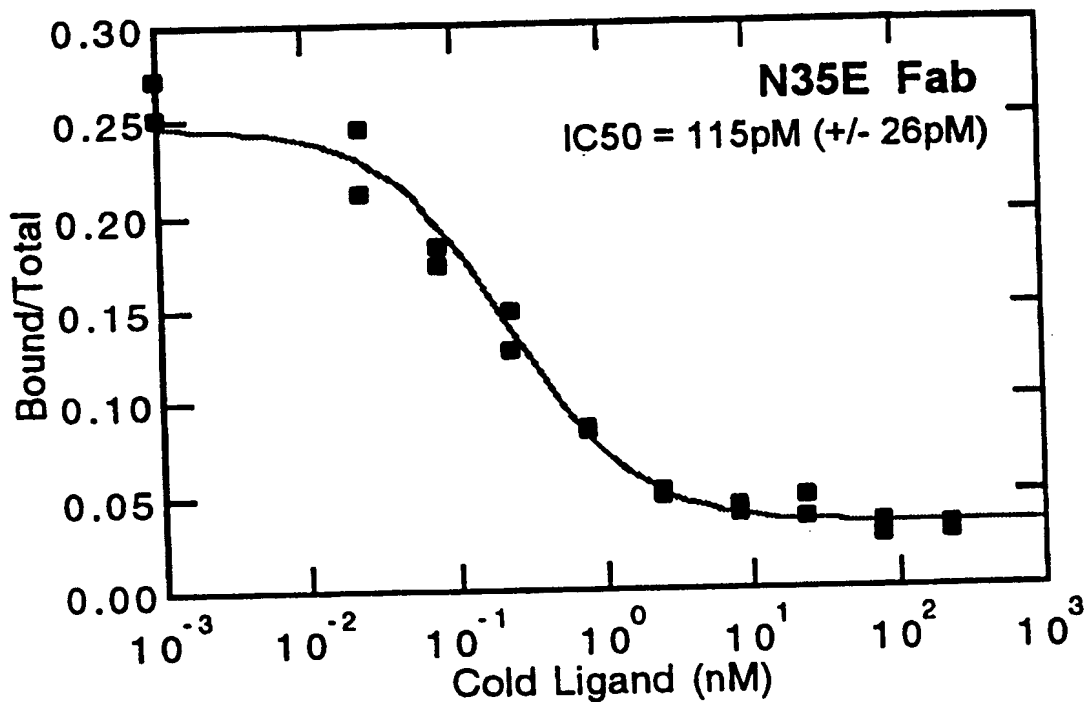


FIG. 43B-3

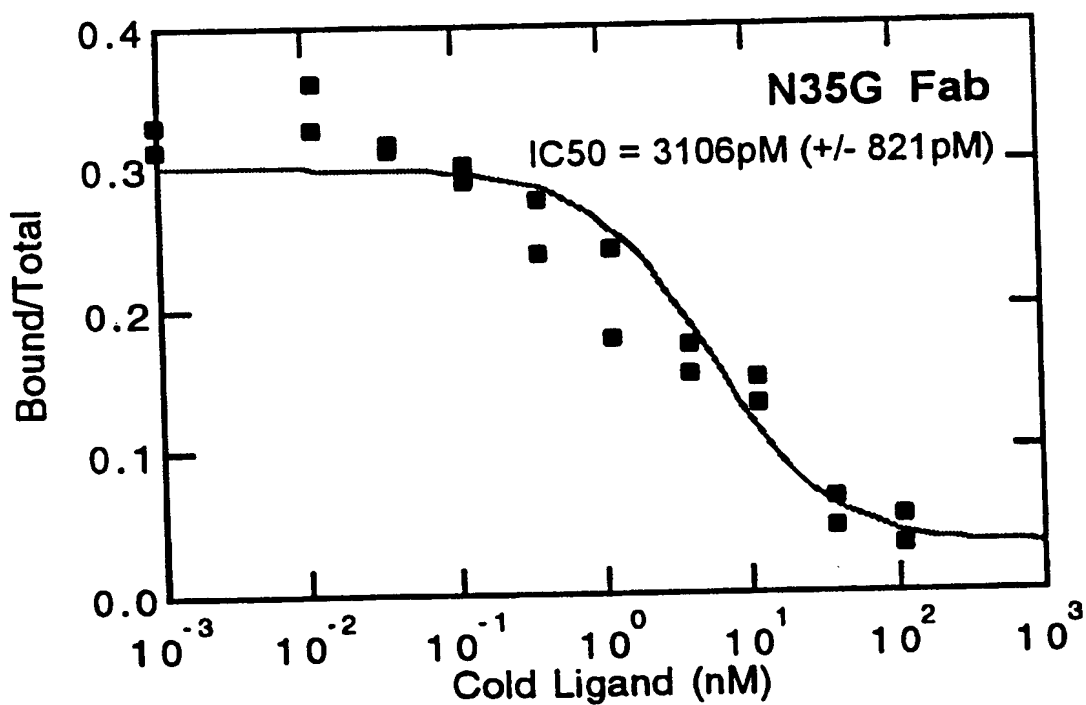
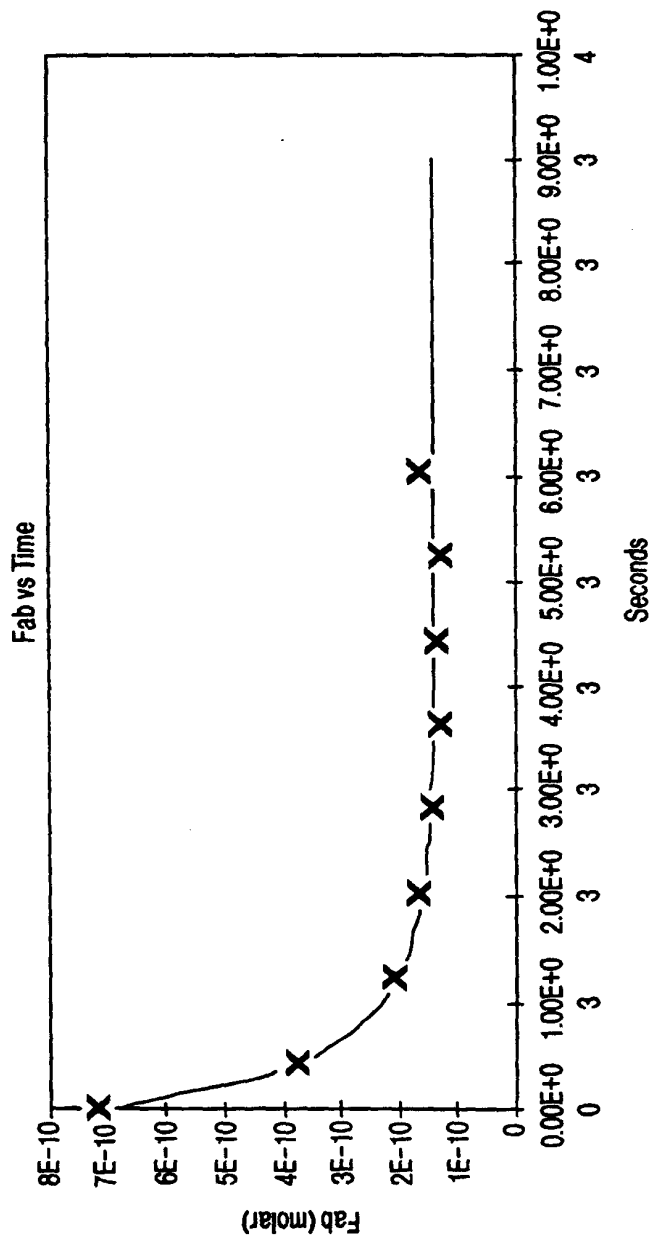


FIG. 43B-4

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Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')₂.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab') ₂	2.0x10 ⁶	2.1x10 ⁻⁴	109pM
6G4V11N35E-Fab	4.7x10 ⁶	2.6x10 ⁻⁴	54pM

FIG. 44

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M K K N I A F L L A S M F V F S I A T N
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCGCGCTC TGTGGGCGAT
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A Y A D I Q M T Q S P S S L S A S V G D
 121 AGGGTCACCA TCACCTGCAG GTCAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA
 18 R V T I T C R S S O S L V H G I G E T Y
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
 AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L H W Y Q Q K P G K A P K L L I Y K V S
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N R F S G V P S R F S G S G S G T D F T
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTT ACAGAGTACT
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L T I S S L Q P E D F A T Y Y C S O S T
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H V P L T F G Q G T K V E I K R T V A A
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
 GGTAAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
 118 P S V F I F P P S D E Q L K S G T A S V
 481 GTGTGCCTGC TGAATAACTT CTATCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
 138 V C L L N N F Y P R E A K V Q W K V D N
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 CGGGAGGTTA GCCCATGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTTG
 158 A L Q S G N S Q E S V T E Q D S K D S T
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
 178 Y S L S S T L T L S K A D Y E K H K V Y
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCTT
 198 A C E V T H Q G L S S P V T K S F N R G
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
 CTCACAATTC GACTAGGAGA TCGGCCTGCG GTAGCACCGG GATCATGCGT TGATCAGCAT
 218 E C Q

FIG. 45

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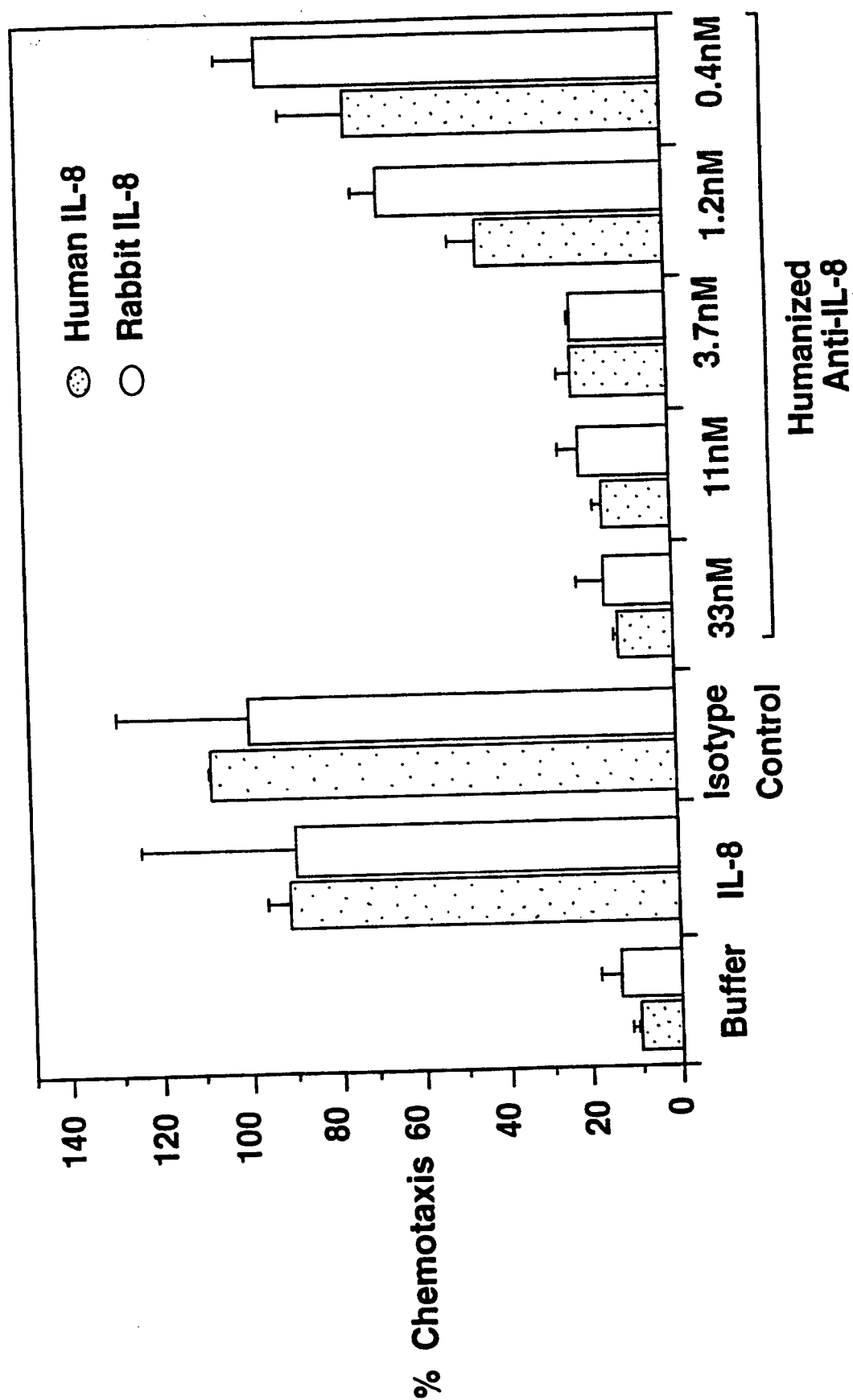


FIG. 46

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N35AH1upr
5'-CTAGTGCAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTCCTTC-3'

N35AH1lwr
5'-TCGAGAAGGAGTAGCCAGAAGCTGCACAGGACAAACGGAGTGAGCCCCCTGGCTGCACCAAGGCCACCGCCAGACTGCAC-3'

Bold indicates nucleotide change destroying PvuII site.

FIG. 47

[illegible]

FIG. 48A

FIG. 48C

```
scrFI
mvaI
ecoRII
dsaV
bstNI
apyI[d
```

```

scrFI
mval
ecorII
dsav
bstNI
apyI[dcn+]
sau96I
avail
asul mnlI sfanI accI mboII
sfanI mboII
alul
1001 AGGTCAGGA GGAAAAAGC ATCAAGTATA AGTTGAAGT CTACGAGAGG AAGACTAAC AGAAGATGC TTTCAGGTC TCTGCTCCCC TCCTAAAGCT
TCCAGGTCCT CCTTTTCCG TAGTTCATAT TCAAACTCA GATGCTCTTC TTTCTGATTG TCCTTCTACG AAAGTTCAAG AGACGAGGG AGGATTTCGA
^END DHFR

```

[illegible]

FIG. 48D

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66E160-4095E60

1201 ATACGATTAA GGTGACACTA TAGATAACAT CCACCTTTGCC TTTCTCTCCA CAGGTGTCCA CTCCAGGTC CAACCTGCACC TCGGTTCTAT CGATTGAAT
TATGCTAAT CCACCTGTGAT ATCTATTGTA GGTGAACCG AAGAGAGGT GTCCACAGGT
seq from PRK6G425VH: Cla-AvrII^

1301 CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGTGCA
GGTGGTACCC TACCAGTACA TAGTAGGAAA AAGATCATCG TTGACGTTGA CCTCATGTAA GTCTTCAAGT CGATCACGTC AGACCGCCAC CGGACCACGT
E V Q L V Q S G G L V Q

1

1401 GCCAGGGGCG TCACTCCGTT TGTCTGTGCG AGCTTCTGCG TACTCTTCT CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCGGGTAA GGCCTGGAA
CGGTCCCCCG AGTGAGGCAA ACAGGACACG TCGAAGACCG ATGAGGACCG GTCTAGTATGAT ATACGTGACC CAGGAGTCC GGGGCCCATT CCGGACCTT
14 P G G S L R L S C A A S G Y S F S S H Y M H W V R Q A P G K G L E

FIG. 48E

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bslI
 sau3AI
 mboI/ndeII[dam-]
 dpnI[dam+]
 dpnII[dam-]
 alvi[dam-] hphI
 1501 TGGGTTGGAT ATATTGATCC TTCCAATGGT GAACTACCT ATAATCAAAA GTTCAAGGCG CGTTTCACCT TATCTCGGA CAACCTCCAAA AACACAGCAT
 ACCCAACCTA TATACTAGG AAGTTACCA CTTTGATGCA TATTAGTTT CAAGTCCCG GCAAGTGAA ATAGAGCGCT GTTGAAGTTT TTGTGTCGTA
 47 W V G Y I D P S N G E T T Y N Q K F K G R F T L S R D N S K N T A Y
 scfI
 pstI
 bsgI
 bspMI
 1601 ACCTGCAGAT GAACAGCCTG CGTGCTCAGG ACACCTGCCG CTATTACTGT GCAAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG
 TGGACGTCTA CTTGTGGGAC GCACGACTCC TGTGACGGCA GATAATGACA CGTTCTCCCG TAATAGCGAT GTTACCACCTG ACCAAGAGC TGCAGACCCC
 81 L Q M N S L R A E D T A V Y Y C A R G D Y R Y N G D W F F D V W G
 hinII/acyI
 ahaiI/bsaHI
 aatII
 bsrI
 maeIII
 hphI
 mboII maeII
 taqI
 scrFI
 mvaI
 ecorII
 dsav
 bstNI
 sau96I
 nlaIV
 hglJII
 bsp1286
 esp3I
 bsmBI
 scrFI
 mvaI
 ecorII
 dsav
 bstNI hphI
 mnlI
 bsaJI
 apyI[dcm+] bsaJI
 bsaJI maeIII bseRI mnlI
 bsaJI bsmAI haeIII/pali haeIII/draII
 nlaIV bstEII bsmAI haeIII/pali eco109I/draII
 1701 TCAAGGAACC CTGGTCACCG TCTCCTCGG CTCACCAAG GGCCCATCGG TCTTCCCCTT GCACCCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC
 AGTTCTTGG GACCACTGGC AGAGGAGCCG GAGGTGGTTC CCGGTAGCC AGAAGGGGA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTGCGCCG
 114 Q G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A
 hglAI/aspHI
 bsp1286
 bseRI
 apyI[dcm+] mnlI
 bmyI mnlI
 bmyI mnlI
 CCTCTGGGGG CACAGCGGCC
 GGAGACCCCC GTGTGCGCCG
 asuI
 fnu4HI
 bsoFI
 bsp1286 aciI bsaJI
 bmyI nspBII apyI[dcm+]

FIG. 48F

[illegible]

FIG. 48G

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sau96I
nlaIV
mspI
hpaII
scrFI
nclI
dsav
sau3AI auaII nlaIII
mboI/ndeII[dam-] nspI
nlaII caulI mnlI nspHI
rcal dpmI[dam+] ddelI mslI
mnlI dpmII[dam-] eco8II maeII
mslI bspHI[dam-] asuI bsu36I/mstII/sauI
earI/ksp632I bsaJI mslI bspHI[dam-] asuI bsu36I/mstII/sauI
2101 CTCCTCCCCC CAANAACCCAA GGACACCTC ATGATCTCCC GGACCCCTGA GGTCACTGC GTGTGGTGG ACCTGAGCCA CGAAGACCCT GAGGTCAAGT
GAGAAGGGGG GTTTGGGTT CCTGTGGGAG TACTAGAGGG CCTGGGGACT CCAGTGACG CACCACCACC TGCACTCGGT GCTTCTGGGA CTCCAGTTCA
247 L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F

acII
thai
fnuDII/mvni
bstUI
bsh1236I
sacII/sstII
nspBII
kspI
dsal
bsaJI
acII
fnu4HI mnlI rsaI csp6I maeII bsaAI
rsal csp6I maeII bsaAI
rsal csp6I maeII bsaAI
hphI hgaI mnlI
2201 TCAACTGGTA CGTGGACGGC GTGAGGTGC ATAATGCCAA GACAAGCCG CGGAGGAGC AGTACAACAG CACGTACCGT GTGTACCGT TCCTCACCGT
AGTTGACCAT GCACCTGCCG CACCTCCACG TATTACGGTT CTGTTTCGGC GCCCTCCTCG TCATGTTGTC GTGCATGGCA CACCAGTCGC AGGAGTGCCA
281 N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V

maeII
rsal csp6I
bsrI bsaAI
2301 TCAACTGGTA CGTGGACGGC GTGAGGTGC ATAATGCCAA GACAAGCCG CGGAGGAGC AGTACAACAG CACGTACCGT GTGTACCGT TCCTCACCGT
AGTTGACCAT GCACCTGCCG CACCTCCACG TATTACGGTT CTGTTTCGGC GCCCTCCTCG TCATGTTGTC GTGCATGGCA CACCAGTCGC AGGAGTGCCA
314 L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G

scrFI
mvaI
corII
dsav
econI bstNI bsrI
bslI apyI[dcm+]
2301 CCTGCACCCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGTCTCCA ACAAGCCCT CCAGCCCCC ATCGAGAAA CCATCTCCAA AGCCAAAGGG
GGAGGTGGTC CTGACCGACT TACCGTTCCT CATGTTACG CATGTTACG GTTTCGGG TGTTCGGG GGGTCGGGG TAGCTCTTTT GGTAGAGGTT TCGGTTTCCC
314 L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G

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FIG. 48H

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scrFI      nciI      mspI      hpaII      dsav      cauII      xmaI/pspAI      smaI      scrFI      nciI      dsav      cauII      foki      rsaI      csp6I      bsp1407I/bsrGI      bali      bsaJI      mboII      auaI      2401 CAGCCCCGAG AACACAGGT GTACACCTG CCCCATCCC GGAAGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA
GTGGGGCTC TTGGTGCCA CATGTGGAC GGGGGTAGG CCGTCTCTTA CTGGTTCTTG GTCCAGTCGG ACTGGACGGA CCAGTTCCG AAGATAGGT
347 Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S

scrFI      mval      ecorII      dsav      bstNI      apyI[dcm+]      bspMI      scrFI      mval      ecorII      dsav      bstNI      apyI[dcm+]      sexAI      2501 GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACATAC AAGACCACGC CTCCTCGTGT GGTCTCTTCT TOCTCTACAG
CGCTGTAGCG GCACCTCACC CTCTCGTTAC CCGTCGSCCT CTTGTGTATG TTCTGGTGG GAGGGCACCA CCTGAGGCTG CCGAGGAAGA AGGAGATGTC
381 D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S

mspi      hpaII      fnu4HI      bsoFI      bsvI      bsrDI      mali      bsaJI      2601 CAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT GTCCTGTGAT GCATGAGGCT CTGCACRACC ACTACACGCA GAAGAGCCTC
GTTCGAGTGG CACCTGTTCT CGTCCACCGT CGTCCCTTGG CAGAAGAGTA CAGGCACTA CGTACTCCGA GACGTGTTGG TGATGTGCGT CTCTCTCGGAG
414 K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L

mboII      bpuAI      maelI      xmnI      bbsI      asp700      nlaIII      sfanI      mnlI      ppulOI      nslI/avaII      nlaIII      sapi      mboII      mnlI      earI/ksp632I

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FIG. 48I

FIG. 48J

FIG. 48K

FIG. 48L

FIG. 48M

FIG. 48N

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      scrFI
      mvaI
      ecorII
      dsav
      bstNI
      apyI[dcn+]
      mnlI
      bslI
      rsaI
      csp6I
      4101 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCAGGAGA GTGTACAGA GCAGGACAGC AAGACAGCA CCTACAGCCT CAGCAGCACC
      TCATGTCACC TTCCACCTAT TGGGGGAGGT TAGCCCATG TAGCCCTCT AGGTCCTCT CACAGTGTCT CGTCTGTCG TTCCTGTCG GATGTCGGA GTCGTGTCG
      151 V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
      fnu4HI
      ddeI bsoFI
      scfI mnlI bbvI
      4201 CTGACGCTGA GGAAGCAGA CTACGAGRAA CACAAAGTCT ACGGCTGCGA AGTCACCAT AGTCGCTGTA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
      GACTGCGACT CGTTTCGTCT GATGCTCTT GTGTTTCAGA TGGGAGGCT TCAGTGGGTA GTCCCGGACT CGAGGGGCA GTGTTCTCG AAGTTGTCCT
      184 L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G
      ddeI
      cellI/espI
      blpI/bp1102I
      hgaI
      4301 GAGAGTGTA AGCTTGCCCG CCATGGCCCA ACTGTGTTAT TGCAGCTTAT AATGTTTACA AATAAGCAA TAGCATCACA AATTCACAA ATAAAGCATT
      CTCTCACAAT TCGRACCGC GGTACCGGT TGAACAATA ACGTCGAATA TTACCAATGT TTATTTCGTT ATCGTAGTGT TTAAGTGT TATTTCGTAA
      218 E C O
      sstI
      sacI
      hgiII
      hgiAI/aspHI
      eciI36II
      bspI286
      bsiHKA I
      bmyI
      ddeI cac8I
      haeIII/palI
      sau96I aluI
      asuI banII
      hphI
      ecoO109I/draII
      maeIII aluI
      accI cac8I
      4401 CTGACGCTGA GGAAGCAGA CTACGAGRAA CACAAAGTCT ACGGCTGCGA AGTCACCAT AGTCGCTGTA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
      GACTGCGACT CGTTTCGTCT GATGCTCTT GTGTTTCAGA TGGGAGGCT TCAGTGGGTA GTCCCGGACT CGAGGGGCA GTGTTCTCG AAGTTGTCCT
      218 L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G
      sau96I
      aciI haeIII/palI
      fnu4HI asuI
      bsoFI nlaIII
      sfiI styI
      aluI haeIII/palI
      hindIII bglI ncoI
      tru9I eaeI dsal
      maeI cfrI bsaJI
      4501 GAGAGTGTA AGCTTGCCCG CCATGGCCCA ACTGTGTTAT TGCAGCTTAT AATGTTTACA AATAAGCAA TAGCATCACA AATTCACAA ATAAAGCATT
      CTCTCACAAT TCGRACCGC GGTACCGGT TGAACAATA ACGTCGAATA TTACCAATGT TTATTTCGTT ATCGTAGTGT TTAAGTGT TATTTCGTAA
      218 E C O
      fnu4HI
      ddeI bsoFI
      scfI mnlI bbvI
      4601 GAGAGTGTA AGCTTGCCCG CCATGGCCCA ACTGTGTTAT TGCAGCTTAT AATGTTTACA AATAAGCAA TAGCATCACA AATTCACAA ATAAAGCATT
      CTCTCACAAT TCGRACCGC GGTACCGGT TGAACAATA ACGTCGAATA TTACCAATGT TTATTTCGTT ATCGTAGTGT TTAAGTGT TATTTCGTAA
      218 E C O
      sfaNI apoI

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FIG. 480

FIG. 48P

[illegible]

FIG. 48Q

FIG. 48B

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mspI nlaIV hgiIII hgiIII nlaIV
 hpaII hgiIII hgiIII hgiIII hgiIII
 naeI bsp1286 bmyI bmyI bmyI
 cfr101/bsrFI aluI aluI aluI aluI
 maeII cac8I maeII haeIII/palI maeII pleI
 draIII sau96I draIII hinfI maeII maeII
 bsaAI asuI hphI hphI hphI hphI
 5301 TTCTCGCCA CGTTGCGCG CTTTCCCGT CAGCTCTAA ATCGGGGGT CCCTTAGG TTCCGATT TAAGCTTTAG GTGCTTTAG GCACCTCGAC CCCAAAAAAC
 AAAGAGCGGT GCAAGCGGC GAAAGGGCA GTTCGAGATT TAGCCCCCGA GGAATATCCC AAGCTAAAT CACGAATGC CGTGGAGCTG GGGTTTTTG
 maeII pleI maeII pleI maeII pleI
 draIII sau96I draIII hinfI maeII maeII
 bsaAI asuI hphI hphI hphI hphI
 5401 TTGATTGGG TGATGGTTCA CGTAGTGGG CATCGCCCTG ATAGACGGT TTTCGCCCTT TGAGCTTGA GTCCACGTTT TTTAATAGTG GACTCTGTT
 AACTAAACC ACTACCAAGT GCATCACCG GTAGCGGAC TATCTGCCA AAAGCGGAA ACTGCAACCT CAGGTGCAAG AAATTATCAC CTGAGAACAA
 bslI bslI bslI bslI
 bsaI bsaI bsaI bsaI
 5501 CCAAACTGA ACAACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT AAGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTAA
 GGTTCGACCT TGTGTGAGT TGGGATAGAG CCCGATAGAG CCCGATAGAG AACTAAATA TTCCCTAAAA CGGCTAAAGC CGGATAACCA ATTTTACT CGACTAAT
 hgiAI/aspHI hgiAI/aspHI hgiAI/aspHI hgiAI/aspHI
 bsp1286 bsp1286 bsp1286 bsp1286
 bsiHKA bsiHKA bsiHKA bsiHKA
 bmyI ddeI bmyI ddeI bmyI ddeI bmyI ddeI
 apaLI/snoI rsaI apaLI/snoI rsaI apaLI/snoI rsaI
 alw44I/snoI csp6I alw44I/snoI csp6I alw44I/snoI csp6I
 5601 CAAAATTTA ACGCAATTT TAACAAATA TTAACGTTTA CAATTTTATG GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAATCC
 GTTTTAAAT TGCCTTAA ATTGTTTAT AATTGCAAT AATTGCAAT GTTAAATAT CAGGTGAGAG TCATGTTAGA CGAGACTAGC GGTATCAAT TCGGTTGAGG
 hinPI hinPI hinPI hinPI
 hhaI/cfoI hhaI/cfoI hhaI/cfoI hhaI/cfoI
 thaI thaI thaI thaI
 fnuDII/mvnl fnuDII/mvnl fnuDII/mvnl fnuDII/mvnl
 bstUI bstUI bstUI bstUI
 nspBII bsh1236I nspBII bsh1236I nspBII bsh1236I
 aciI aciI aciI aciI
 maeIII maeIII maeIII maeIII
 maeII bsrI nlaIII hhaI/cfoI maeII bsrI nlaIII hhaI/cfoI
 bsaAI tth111I/aspI bbvI bsaAI tth111I/aspI bbvI bsaAI tth111I/aspI bbvI
 5701 GCTATCGCTA CGTACTGGG TCATGGCTGC GCCCGACAC CCGCCACAC CCGCTGACGC GCTTGTCTGC TCCCGGCATC CGCTTACAGA
 CGATAGCGAT GCACTGACCC AGTACCGACG CGGGGCTGTG GCGGCTGTG GCGGCTGTG GCGGCTGTG GCGGCTGTG GCGGCTGTG

FIG. 48S

5801
5901
6001
6101

FIG. 48T

sau3AI nspBII sau3AI maeII
 mboI/ndeII[dam-] mboI/ndeII[dam-]
 dpnI[dam+] dpnI[dam+] pep1406I
 bstVI/xhoII bstVI/dam-] alwI[dam-] xmnI
 bsrI dpnII[dam-] alwI[dam-] asp700
 bsrI dpnII[dam-] acII bstVI/xhoII mboII
 alwI[dam-] alwI[dam-] acII bstVI/xhoII
 bssSI maeIII taqI alwI[dam-] acII bstVI/xhoII
 CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACCT TTAAGATTCT
 6201 TGCTCACCC AATGTAGCTT GACCTAGAGT TGTGCGCAAT CTAGGAATC TCAAAAGCGG GGCCTTCTTGC AAAAGGTTAC TACTCGTGAA AATTTCARAGA
 scrFI
 acII nciI
 thaI mspI
 fnuDI/mvni hpaII
 bstUI deav
 bsh1236I hinII/acyI acII
 hinPI hgaI cauII mcrI fnu4HI
 hhai/cfoI ahaII/bsaHI bcoI bsiEI bsoFI ddel
 6301 GCTATGTGCG GCGGTATTAT CCGGTGATGA CGCGGGGCAA GAGCAACTCG GTCGCCGCAT ACACATTCTT CAGAATGACT TGGTTGAGTA CTCACCCAGTC
 CGATACACCG CGCCATAATA GGGCACIACCT GCGGCCCGTT CTCGTTGAGC CAGCGGCGTA TGTGATAAGA GTCTTACTGA ACCAACTCAT GAGTGGTTCAG
 sau3AI
 mboI/ndeII[dam-]
 dpnI[dam+] dpnII[dam-]
 pvuI/bspCI
 mcrI
 bsiEI
 haeIII/palI
 eaeI
 cfrI
 fnu4HI
 bsoFI
 acII
 6401 ACAGAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACACCTGCCG CAACTTACTT CTGACACAACGA
 TAGCTTTTCG TAGAATGCCT ACGTACTCTT CATTCTCTTA ATAGTCTCAG ACGGTATTGG TACTCACTAT TGTGACGCCG GTTGAATGAA GACTGTTGCT
 nlaIII
 sau3AI maeIII mspI
 mboI/ndeII[dam-] sau3AI nlaIV
 dpnI[dam+] mboI/ndeII[dam-] aluI
 dpnII[dam-] dpnI[dam+] hpaII
 nlaIII alwI[dam-] dpnII[dam-] bsaWI
 6501 TCGGAGGACC GAAGAGCTA ACCGCTTTTT TGCACAACAT GGGGATCAT GTAACCTGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCAATACCAA
 AGCTCCTGG CTTCCTCGAT TGGCGAAAAA ACGTGTCTGA CCCCCTAGTA CATTGAGCGG AACTAGCAAC CATTGGCCTC GACTTACTTC GGTATGGTTT

FIG. 48U

[illegible]

FIG. 48V

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sau3AI
mboII[dam-]
sau3AI mboI/ndeII[dam-] thaI
mboI/ndeII[dam-] fnuDII/mvni
dplI[dam+] dplI[dam+] bstUI cac8I
dplII[dam-] dplII[dam-] bsh1236I fnu4HI
bstYI/xhoII alwI[dam-] hinPI bsoFI
bstYI/dam-] bstYI/xhoII hhal/cfoI bbvI
alwI[dam-] TTTCTTGAGAT CCTTTTTTC TCGCGTAAT TCGCGTAAT CTGCTGCTTG CAAACAAAAG AACCAAGGCT ACCAGCGGTG GTTGTGTTGC CGGATCAAGA
AGTTTCTAG AGAACTCTA GGAAGAAAAG ACGCGCATTG GACGACGAAC GTTGTGTTT TTTGTGCGCA TGGTC3CCAC CAAACAAACG GCCTAGTTCT
7101 TCAAGGATC TTTCTTGAGAT CCTTTTTTC TCGCGTAAT TCGCGTAAT CTGCTGCTTG CAAACAAAAG AACCAAGGCT ACCAGCGGTG GTTGTGTTGC CGGATCAAGA
AGTTTCTAG AGAACTCTA GGAAGAAAAG ACGCGCATTG GACGACGAAC GTTGTGTTT TTTGTGCGCA TGGTC3CCAC CAAACAAACG GCCTAGTTCT

rmaI haeIII/pall
mael hael
bfaI bsII
7201 GCTACCAACT CTTTTCCGA AGGTAAGTGG CTTACAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAGAAC
CGATGGTGA GAAAAGGCT TOCATTGACC GAATGCTGCT CCGCTCTATG GTTATGACA GGAAGATCAC ATCGGCATCA ATCCGGTGGT GAAGTTCTTG

fnu4HI
bsoFI
bbvI
alwNI[dcM-]
bsrI bsoFI
maeIII bbvI bsrI
7301 TCTGTAGAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT GCGGATAAGT CGTGTCTTAC CGGTTGGAC TCAAGACGAT
AGACATCGTG CCGGATGTAT GGAGCGAGAC GATTAGGACA ATGGTCACCG ACGACGGTCA CCGCTATTCA GCACAGAAATG GCCCAACCTG AGTTCTGCTA

acII
nspBII
fnu4HI
mspI bsoFI
hpaII bbvI mcrI
bsaWI hinPI bsiEI
maeIII hhal/cfoI
7401 AGTTACCGGA TAAGGCGCAG CCGTCGGGCT GAACGGGGG TCGTGTGCACA CAGCCAGCT TGGAGCGAAC GACCTACACC GAAGTGAAT ACCTACAGCG
TCAATGGCCT ATTCCCGCT GCCAGCCCGA CTTGCCCCCC AAGCAGCTGT GTCGGGTGGA ACCTCGCTTG CTGGATGTGG CTTGACTCTA TGGATGTGCG

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FIG. 48W

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666T60"44095E60

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scrFI      mvaI      ecorII      dsav      bstNI      haeII      hinPI      hhaI/cfoI      fnu4HI      fnu4HI      bssSI      hinPI      mnlI      hhaI/cfoI      aluI      apyI[dcM+]
7501 TGAGCATTGA GAAAGGCCA CGCTTCCGA AGGAGAAAG GGGACAGGT ATCCGGTAAG CGGCAGGCTC GGAACAGGAG AGCGACGAG GGAGCTTCCA
ACTCGTAACT CTTTCGGGT GCGAAGGGCT TCCCTCTTTC CGCCTGTCCA TAGGCATTC GCCGTCCAG CCTTGCTCCTC CTCGCTGCTC CCTCGAAGGT

scrFI      mvaI      ecorII      dsav      bstNI      haeII      hinPI      hhaI/cfoI      fnu4HI      fnu4HI      bssSI      hinPI      mnlI      hhaI/cfoI      aluI      apyI[dcM+]
7601 GGGGAAACG CTTGGTATCT TTATAGTCTT GTCCGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTGTG ATGCTCGTC AGGGGGCGCG AGCCTATGGA
CCCCCTTTCG GGACCATAGA AATATCAGGA CAGCCCAAAG CGGTGAGAG TGAACCTGCA GCTAAAACA CTACGAGCAG TCCCCCGCGC TCGGATACCT

scrFI      mvaI      ecorII      dsav      bstNI      haeII      hinPI      hhaI/cfoI      fnu4HI      fnu4HI      bssSI      hinPI      mnlI      hhaI/cfoI      aluI      apyI[dcM+]
7701 AAAACGCCAG CAACGCCGCT TTTTACGGT TCCTGGCCCT TTGCTGCCCT TTTGCTCACA TGTCTTTTCC TCGGTTATCC CCGTATTCG TGGATAACCG
TTTTCGGCTC GTTGGCCCGG AAAATGCCA AGGACCCGGA AACGACCGGA AACGACGCTG ACAGAAAGG ACCTAATAGG GGAATAGAC ACCTATTTGG

scrFI      mvaI      ecorII      dsav      bstNI      haeII      hinPI      hhaI/cfoI      fnu4HI      fnu4HI      bssSI      hinPI      mnlI      hhaI/cfoI      aluI      apyI[dcM+]
7801 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCGCGCAG CGAACGACCG AGCGACGCGA GTCAGTGAGC GAGGAGCGG AGAGCGGCC AATACGCAAA
ATAATGGCGG AAATCACTC GACTATGCGC AGCGGCGTGC GCTTGCTGSC TCGGCTGCTC CAGTCACCTG CTCCTTCGCC TTCTCGCGG TTATCGGTTT

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FIG. 48X

FIG. 48Y

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tru9I
mseI
aseI/asnI/vsPI
xmni
nlaII
asp700
8101 TGACCATGAT TACGAATTAA
ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC): 1690 5947
acc65I(GGTACC): 2969 3967 4529
823 1039 2738 4237
217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070
see hinII
acyI
aflII/bfRI(CTTAAG): 786
aflIII(ACRYGT): 932 7758
ageI(ACCGGT): 1833
ahaII/bsaHI(GRCGYC): 988 1690 1858 5117 5947 6329
ahaII/draI(TTTAA): 696 4935 6290 6982 7001
ahdI/eam1105I(GACNNNNNGTC): 2087 6865
5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
aluI(AGCT):
alw44I/snoI(GTGCAC): 1876 5651 6198 7444

```

FIG. 48Z

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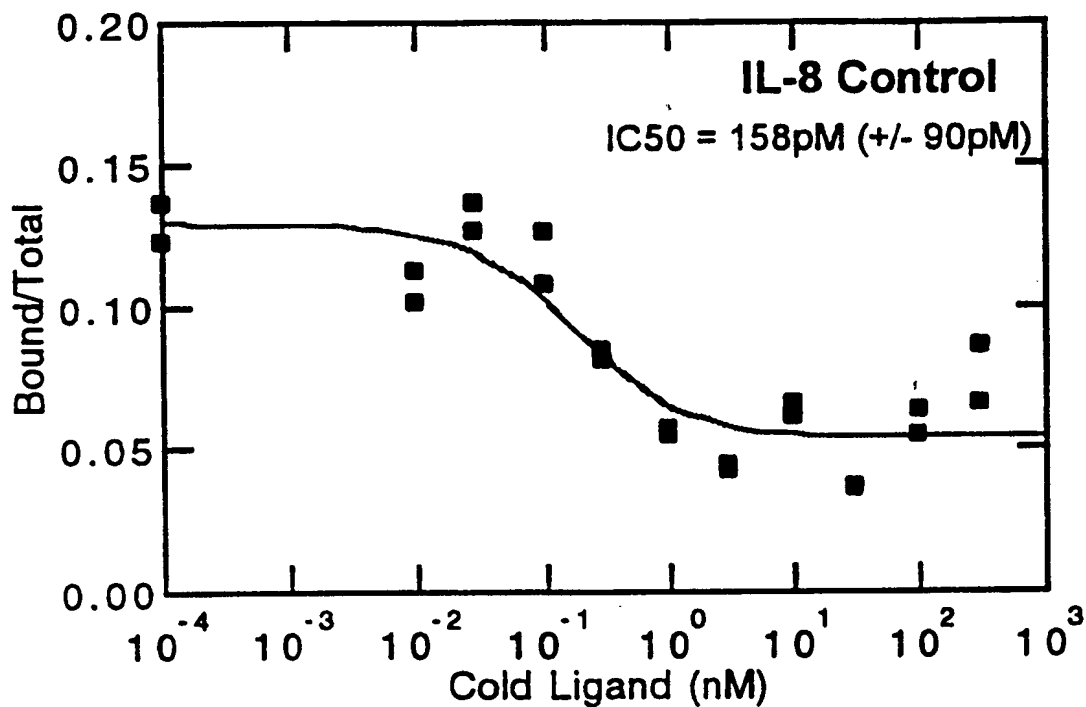


FIG. 49A

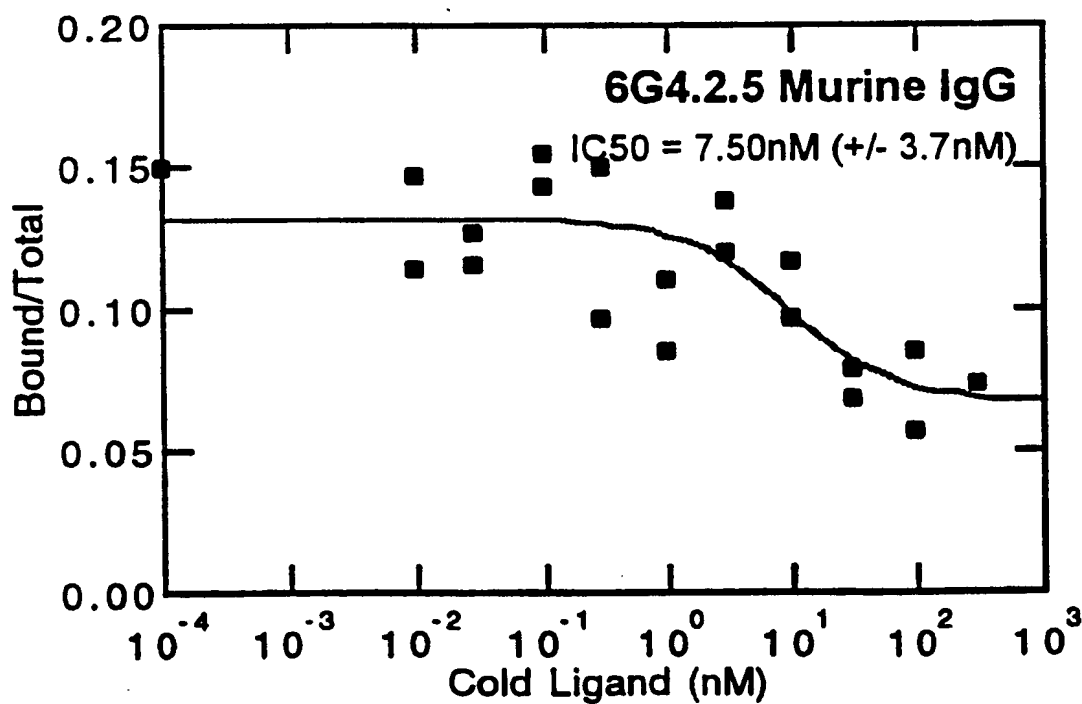


FIG. 49B

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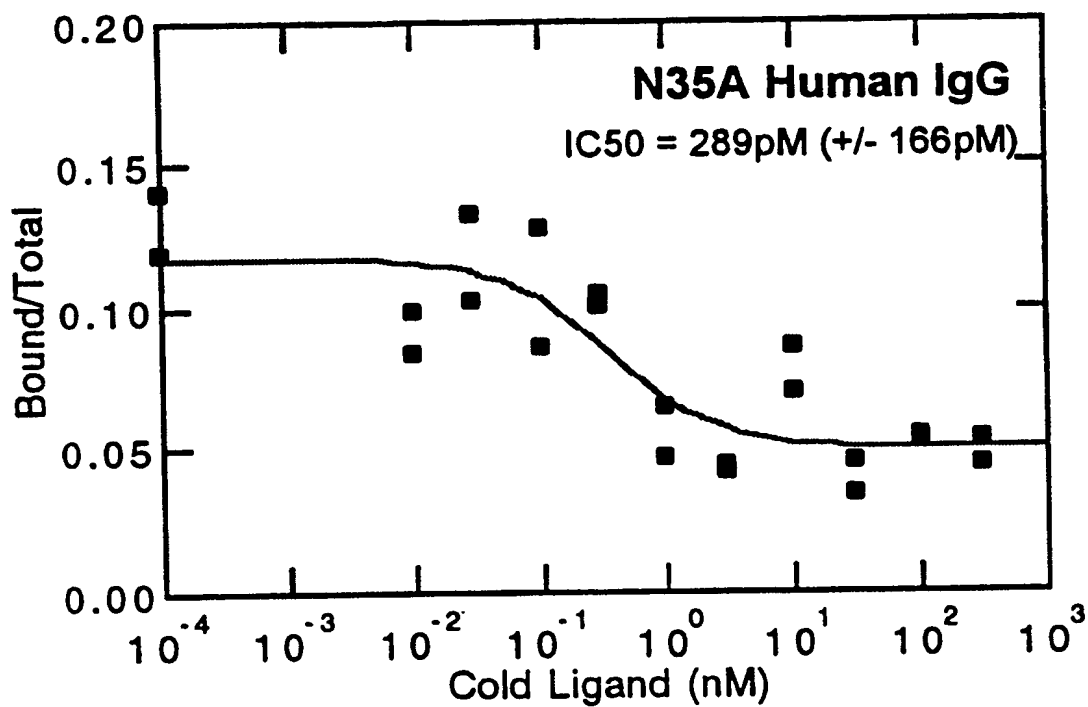


FIG. 49C

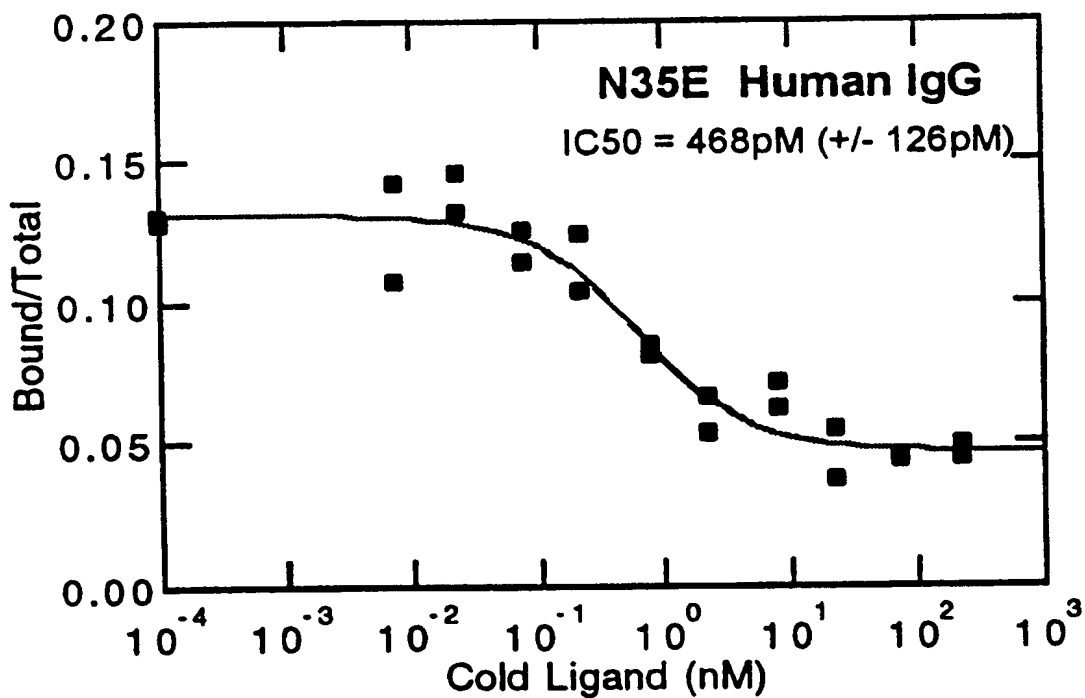


FIG. 49D

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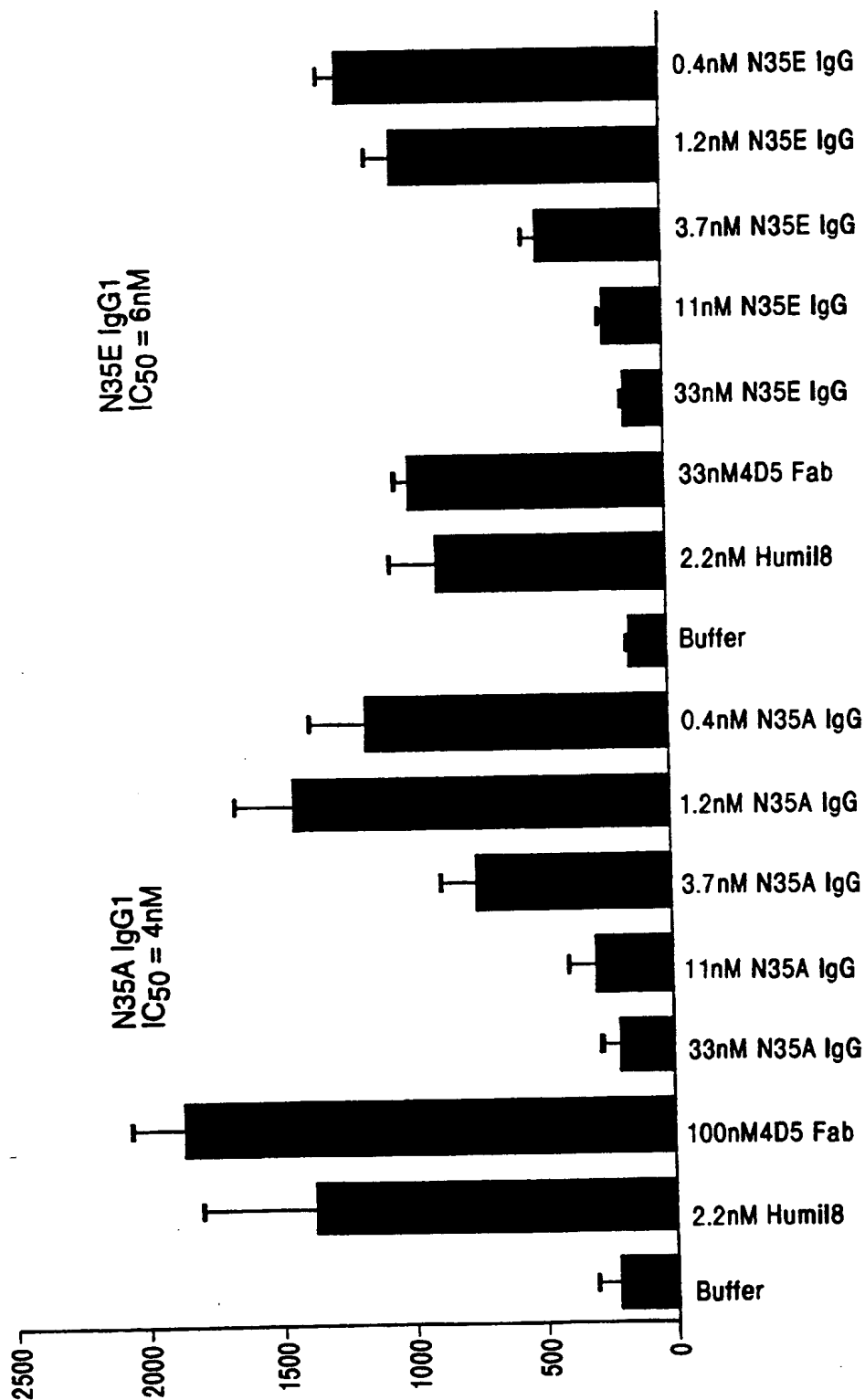


FIG. 50A

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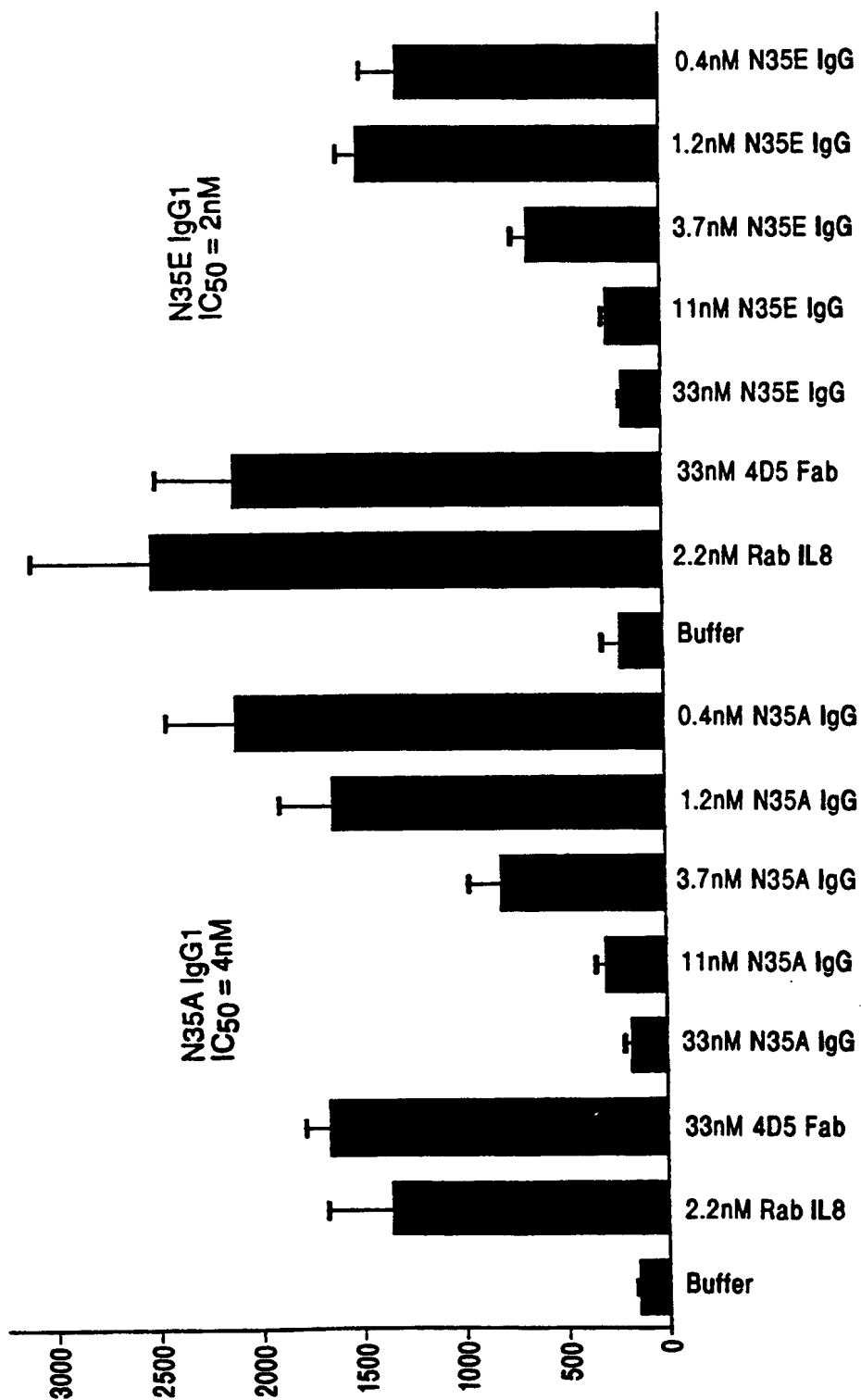
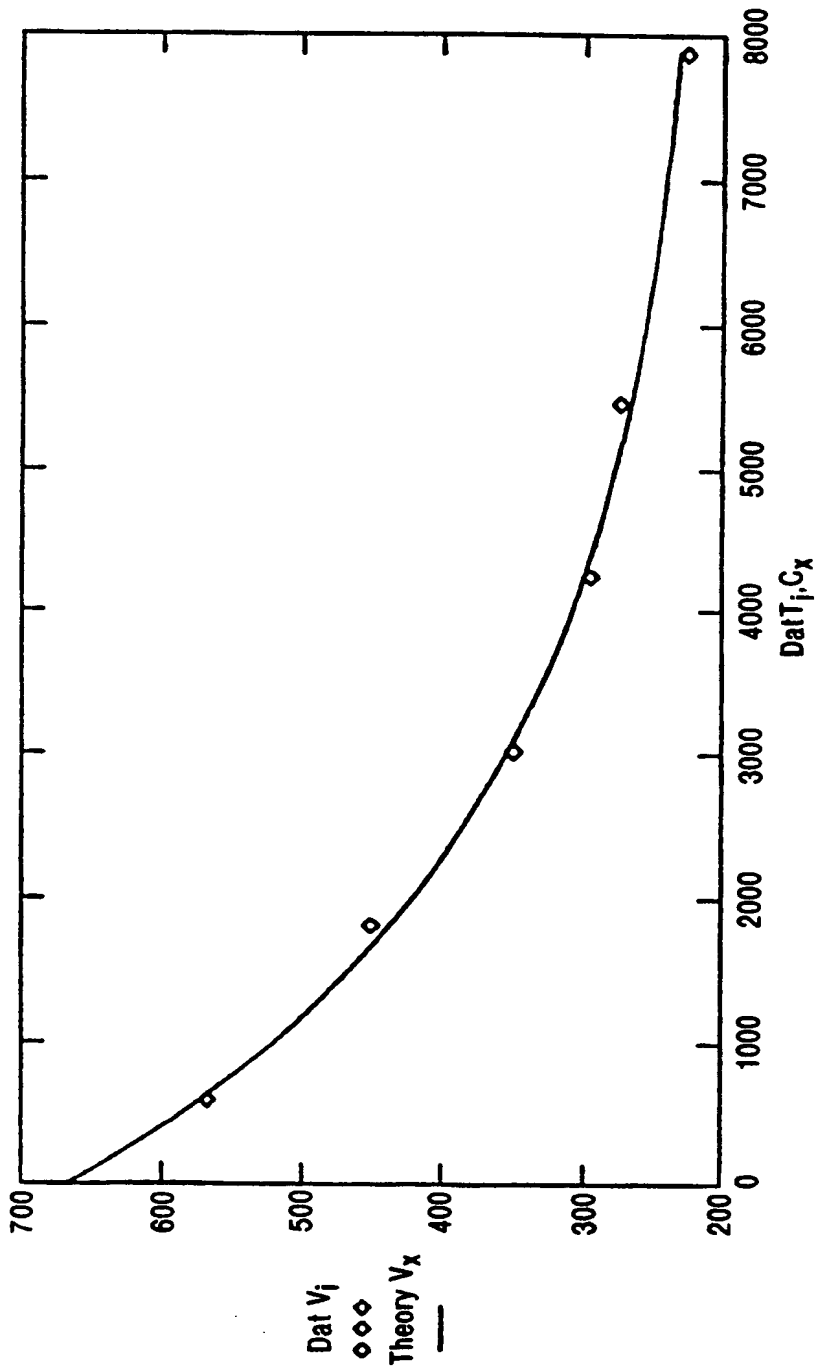


FIG. 50B



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.IgG1

SAMPLE	ka	kd	Kd
Murine 6G4.2.5 IgG2a	8.3x10 ⁵	2.9x10 ⁻⁴	350pM
6G4V11N35A-IgG1	8.7x10 ⁵	7.7x10 ⁻⁵	88pM
6G4V11N35E-IgG1	3.0x10 ⁶	1.4x10 ⁻⁴	49pM

FIG. 51

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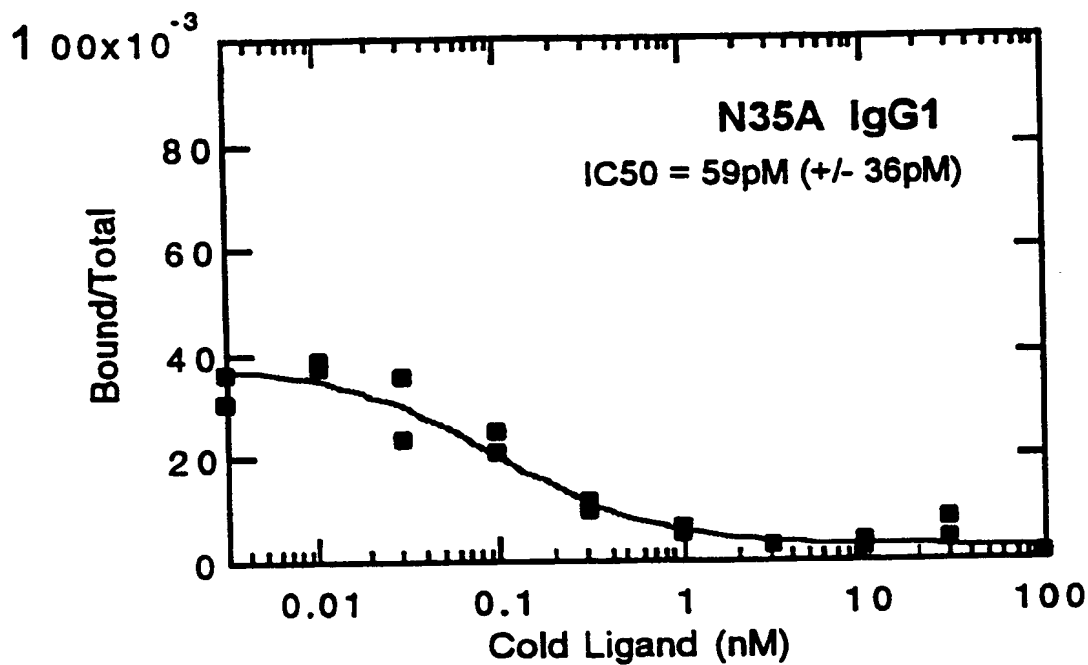


FIG. 52A

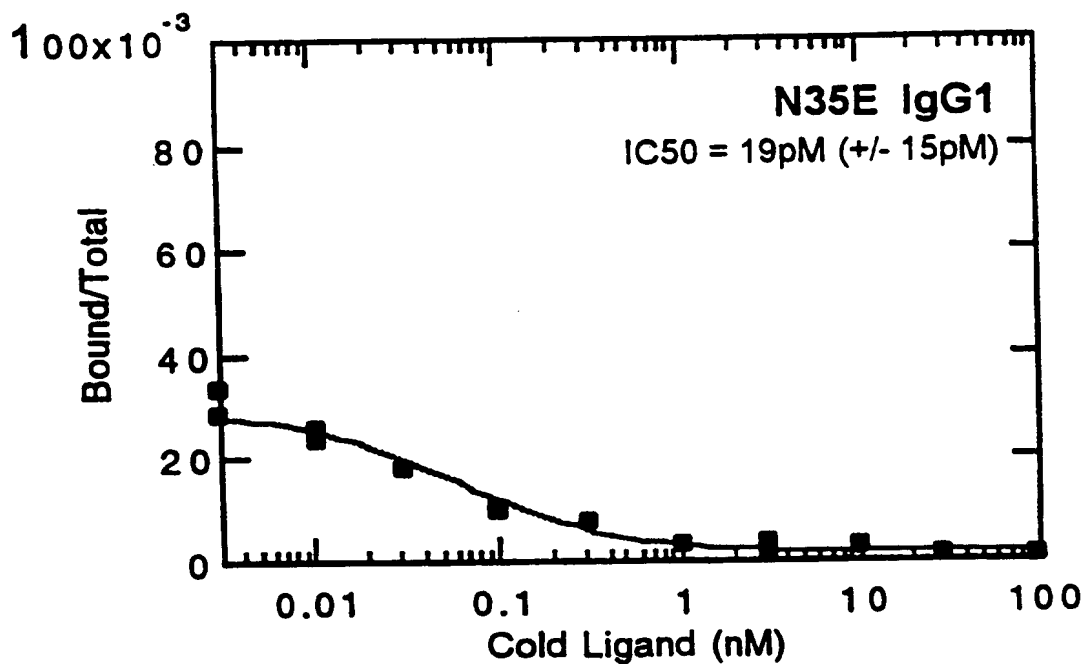
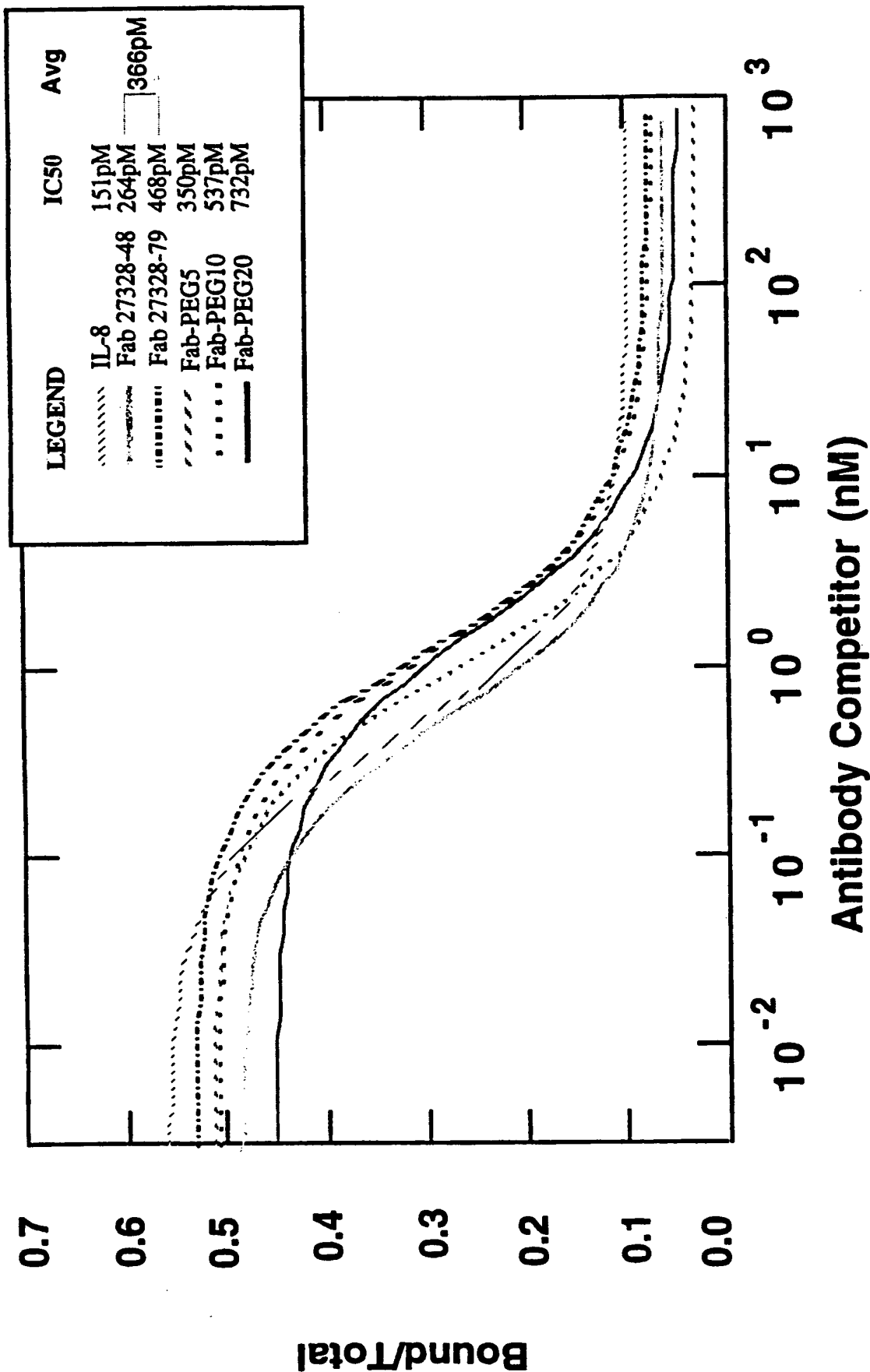


FIG. 52B

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781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
 TTTTCCCATATA GATCTCCAAC TCCACTAAAA TACTTTTCT TATAGCGTAA AGAAGAACGT
 -1 M K K N I A F L L A
 841 TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT
 AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
 -11 S M F V F S I A T N A Y A E V Q L V Q S
 901 GCGGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
 CCGCCACCGG ACCACGTCGG TCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
 8 G G G L V Q P G G S L R L S C A A S G Y
 961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
 AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTTCCC GGACCTTACC
 28 S F S S H Y M H W V R Q A P G K G L E W
 1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
 CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAT GTTCCCGGCA
 48 V G Y I D P S N G E T T Y N O K F K G R
 1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
 AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
 68 F T L S R D N S K N T A Y L Q M N S L R
 1141 GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
 CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCTTAA TAGCGATGTT ACCACTGACC
 88 A E D T A V Y Y C A R G D Y R Y N G D W
 1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
 AAGAAGCTGC AGACCCCACT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
 108 F F D V W G Q G T L V T V S S A S T K G
 1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
 GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC
 128 P S V F P L A P S S K S T S G G T A A L
 1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
 CCGACGGACC AGTTCTCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
 148 G C L V K D Y F P E P V T V S W N S G A
 1381 CTGACCAGCG GCGTGCACAC CTTCCCCGCT GTCCTACAGT CCTCAGGACT CTA CTCCCTC
 GACTGGTCCG CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
 168 L T S G V H T F P A V L Q S S G L Y S L
 1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
 TCGTCGCACC ACTGGCACGG GAGGTCTGCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
 188 S S V V T V P S S S L G T Q T Y I C N V
 1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
 TTAGTGTTTCG GGTCTGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
 208 N H K P S N T K V D K K V E P K S C D K
 1561 ACTCACACAT GCCCGCCGTGA
 TGAGTGTGTA CGGGCGGCACT
 228 T H T C P P O

FIG. 53



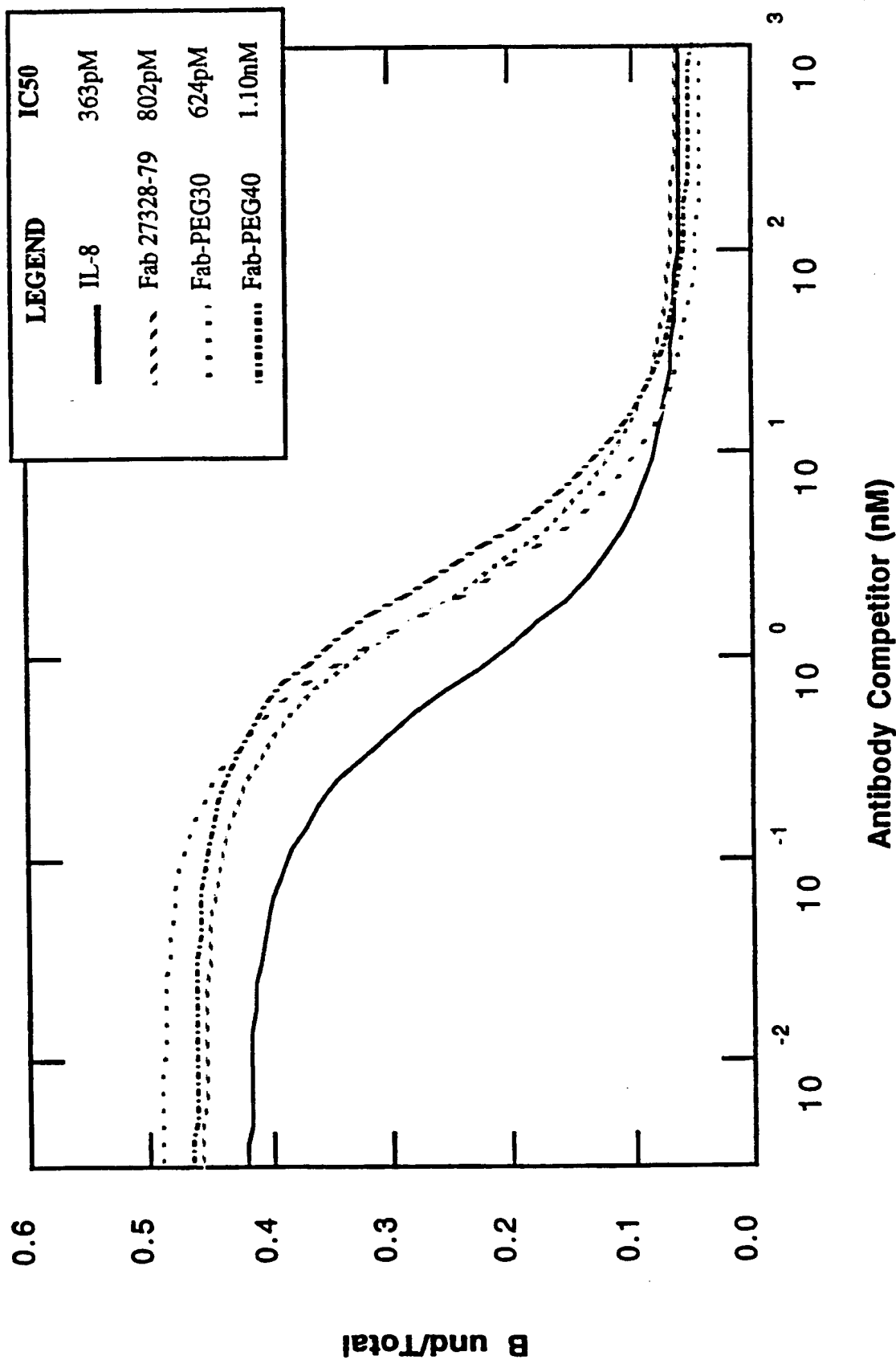
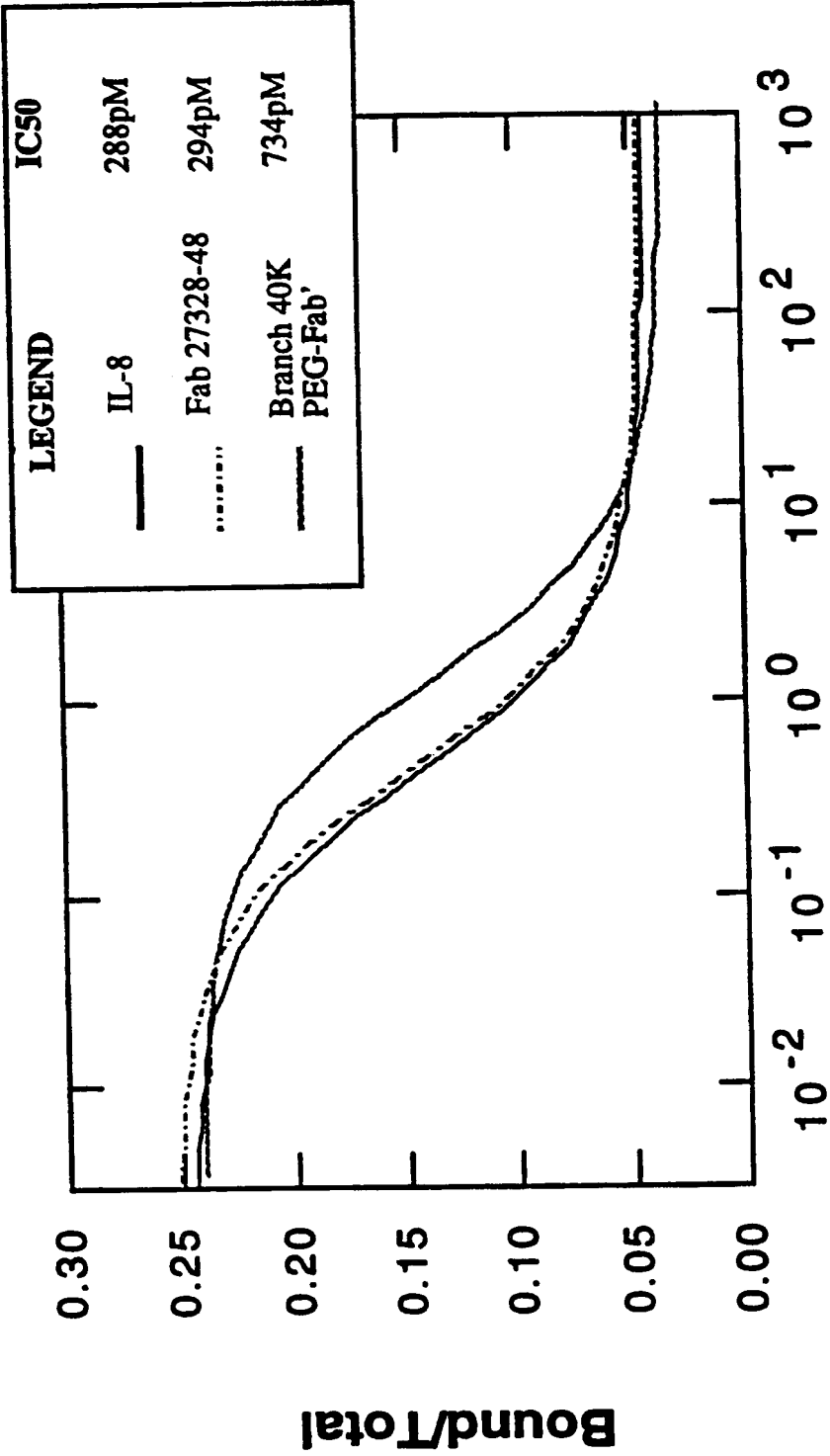


FIG. 54B



Antibody Competitor (nM)

FIG. 54C

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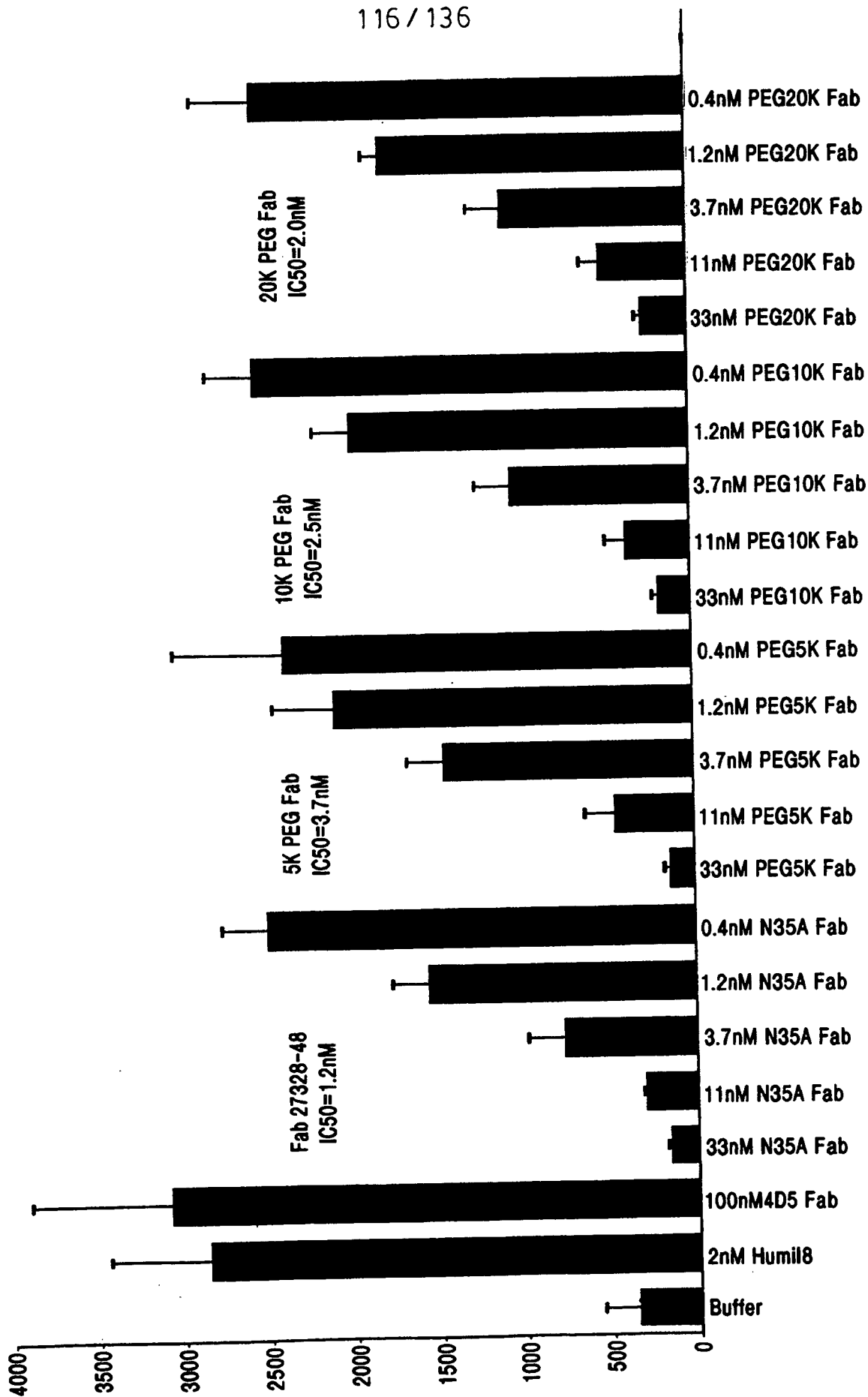


FIG. 55A

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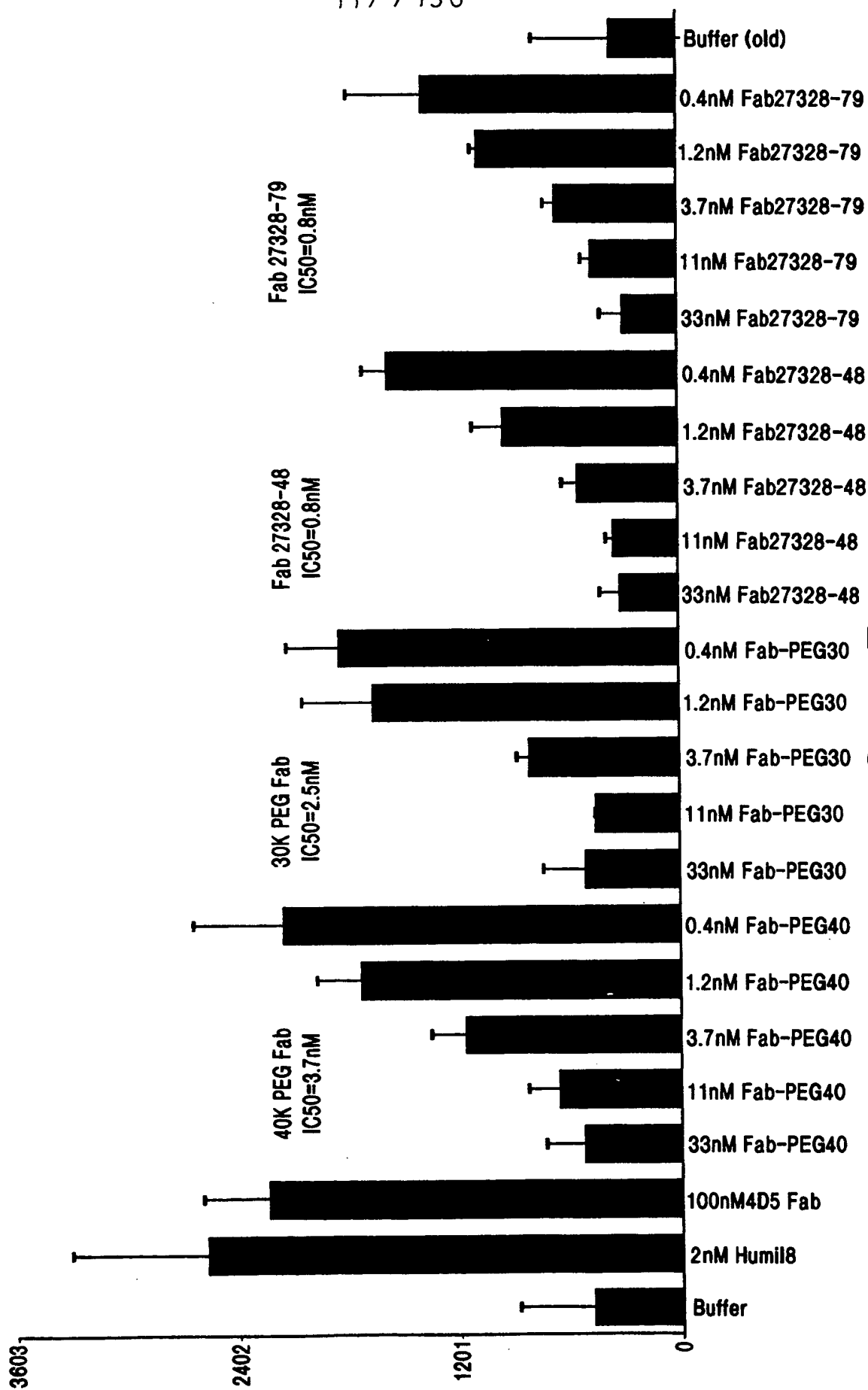


FIG. 55B

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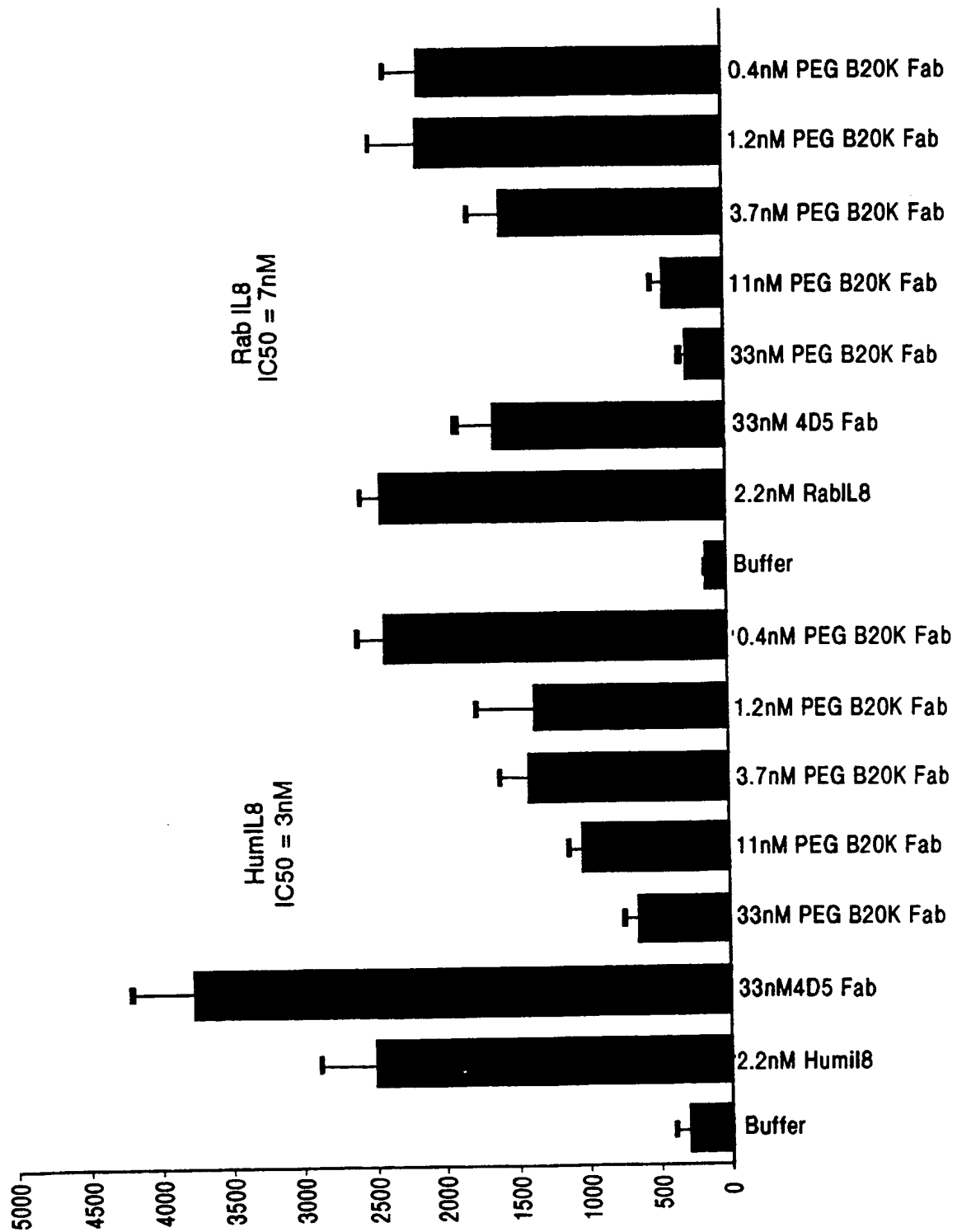
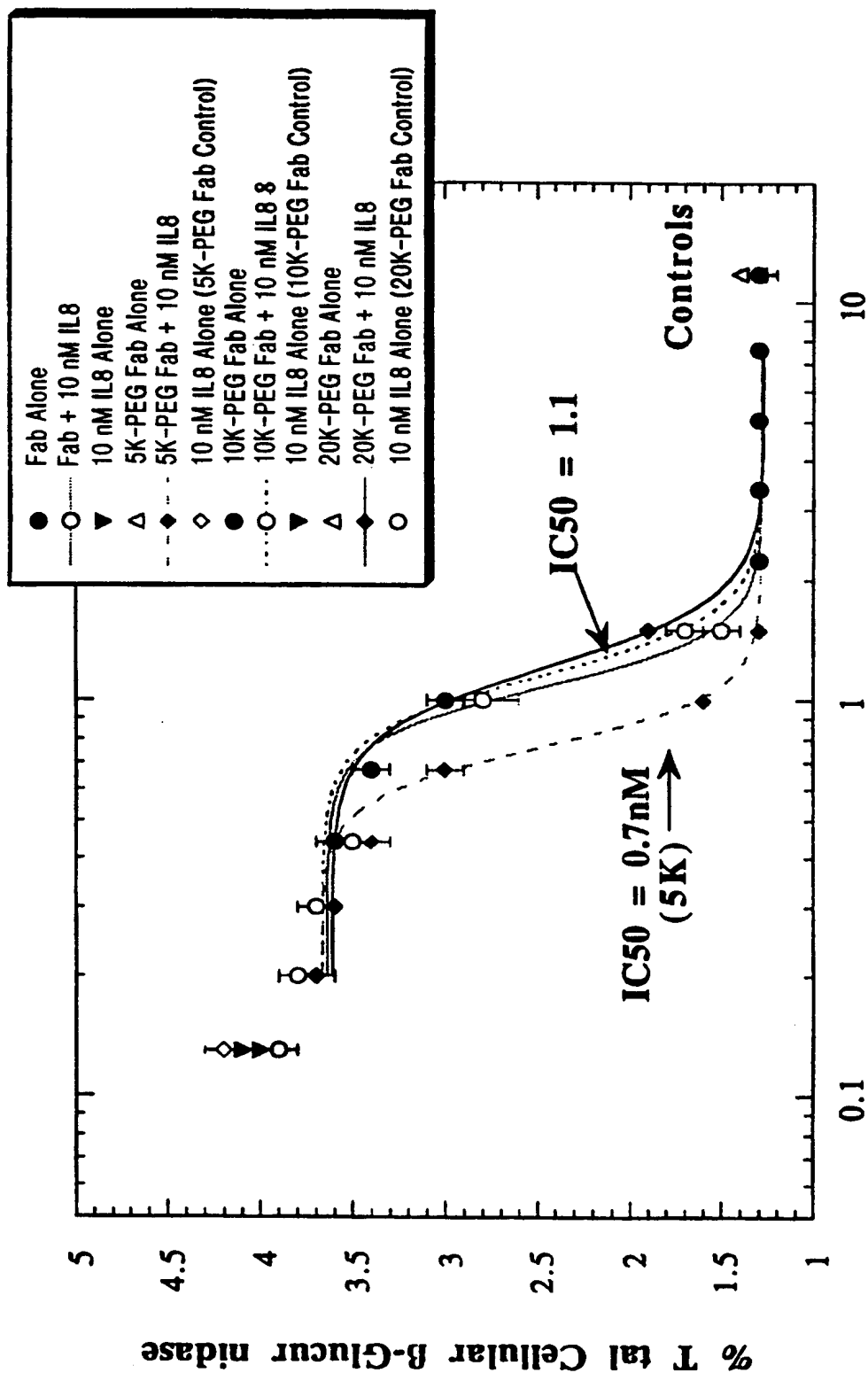


FIG. 55C



Molar Ratio Antibody:IL-8

FIG. 56A

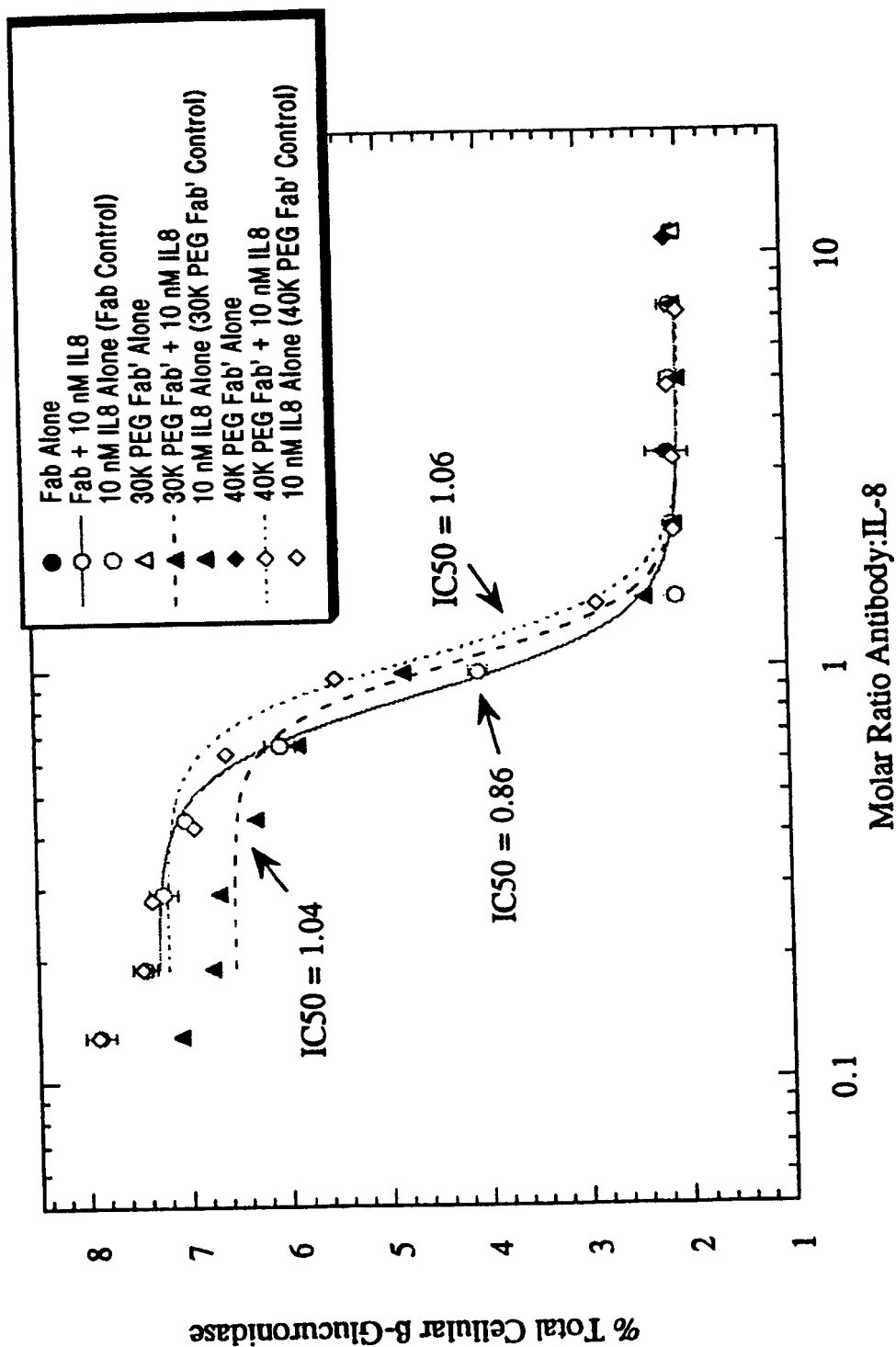
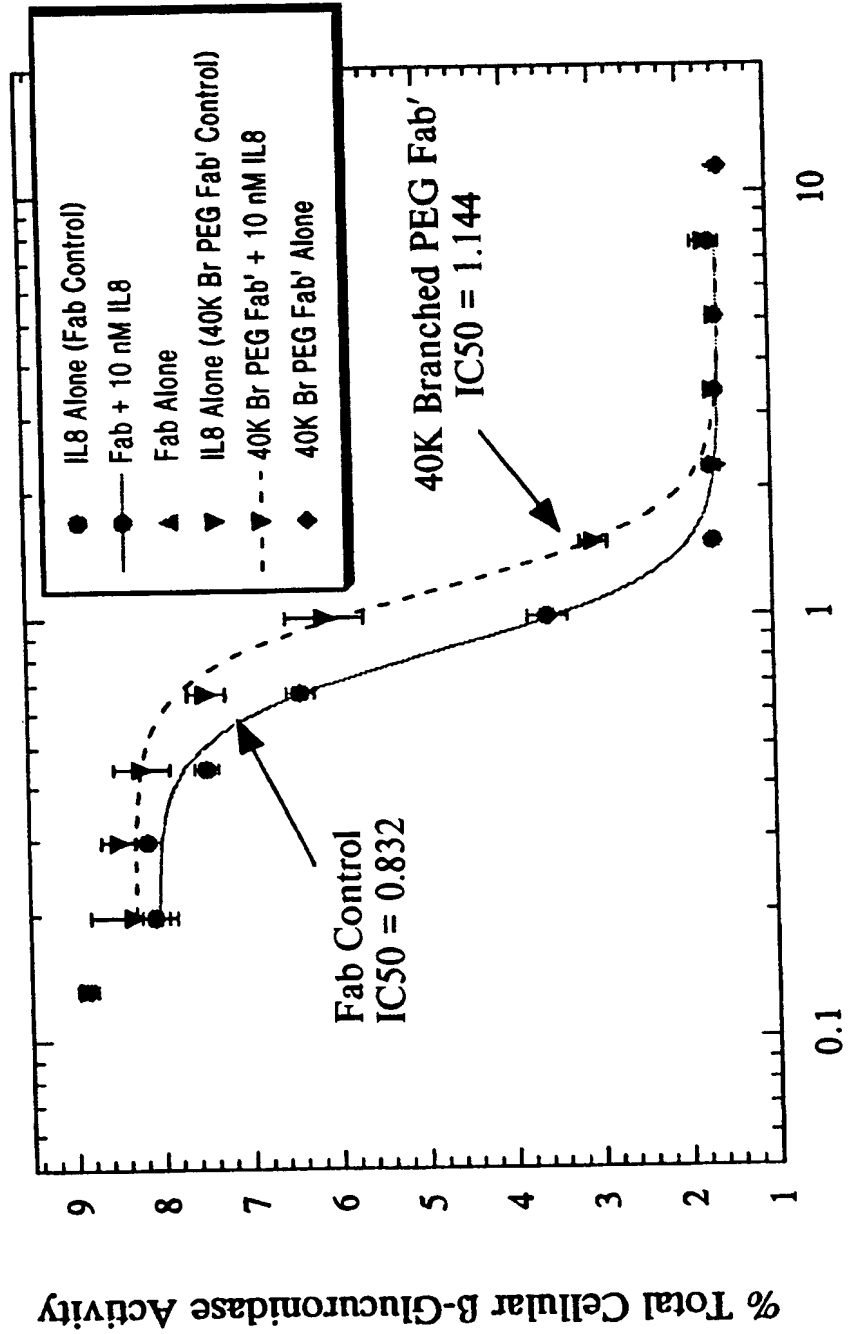


FIG. 56B

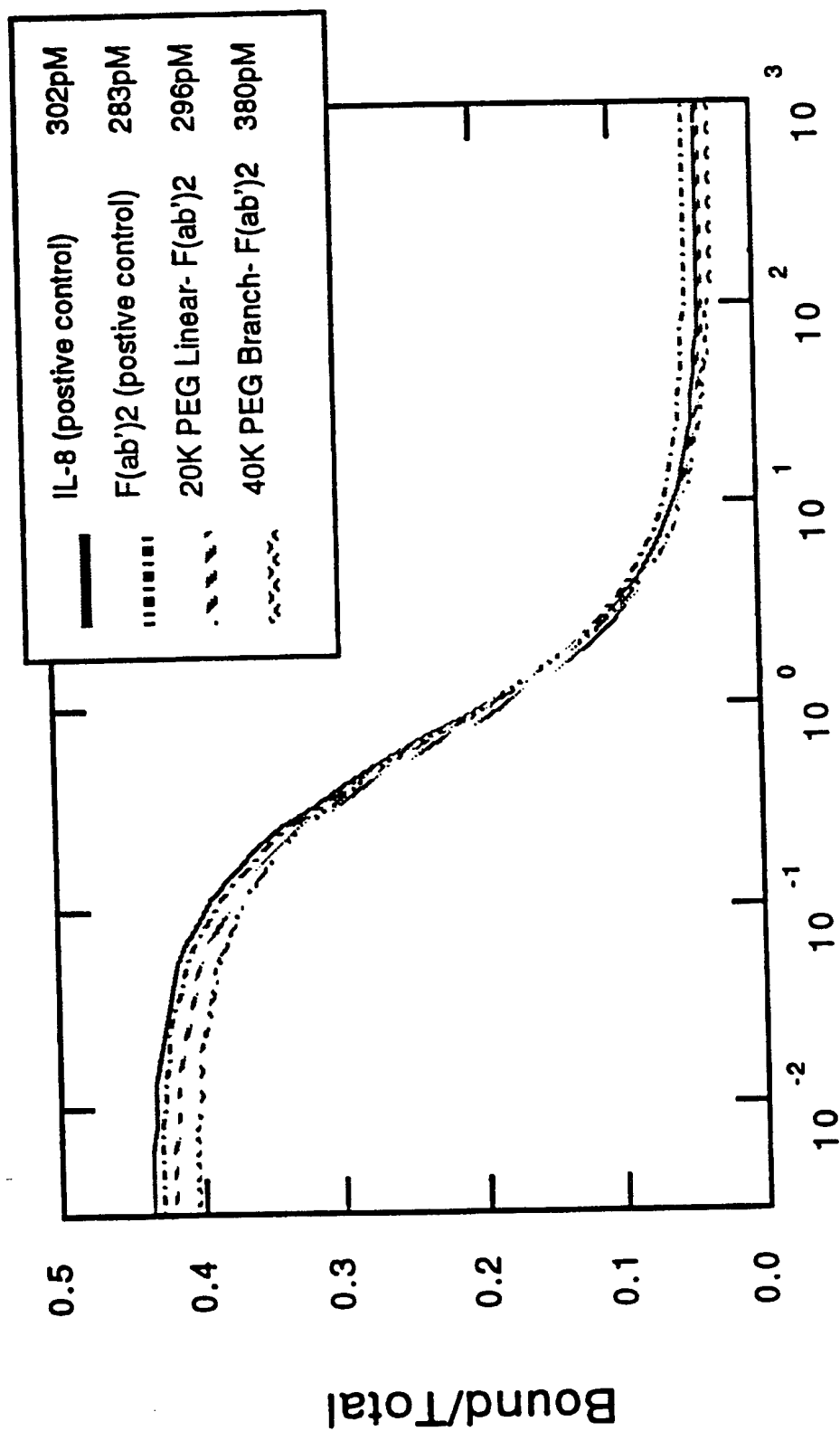
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Molar Ratio Antibody:IL8

FIG. 56C

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Pegylated F(ab')₂ (nM)

FIG. 57A

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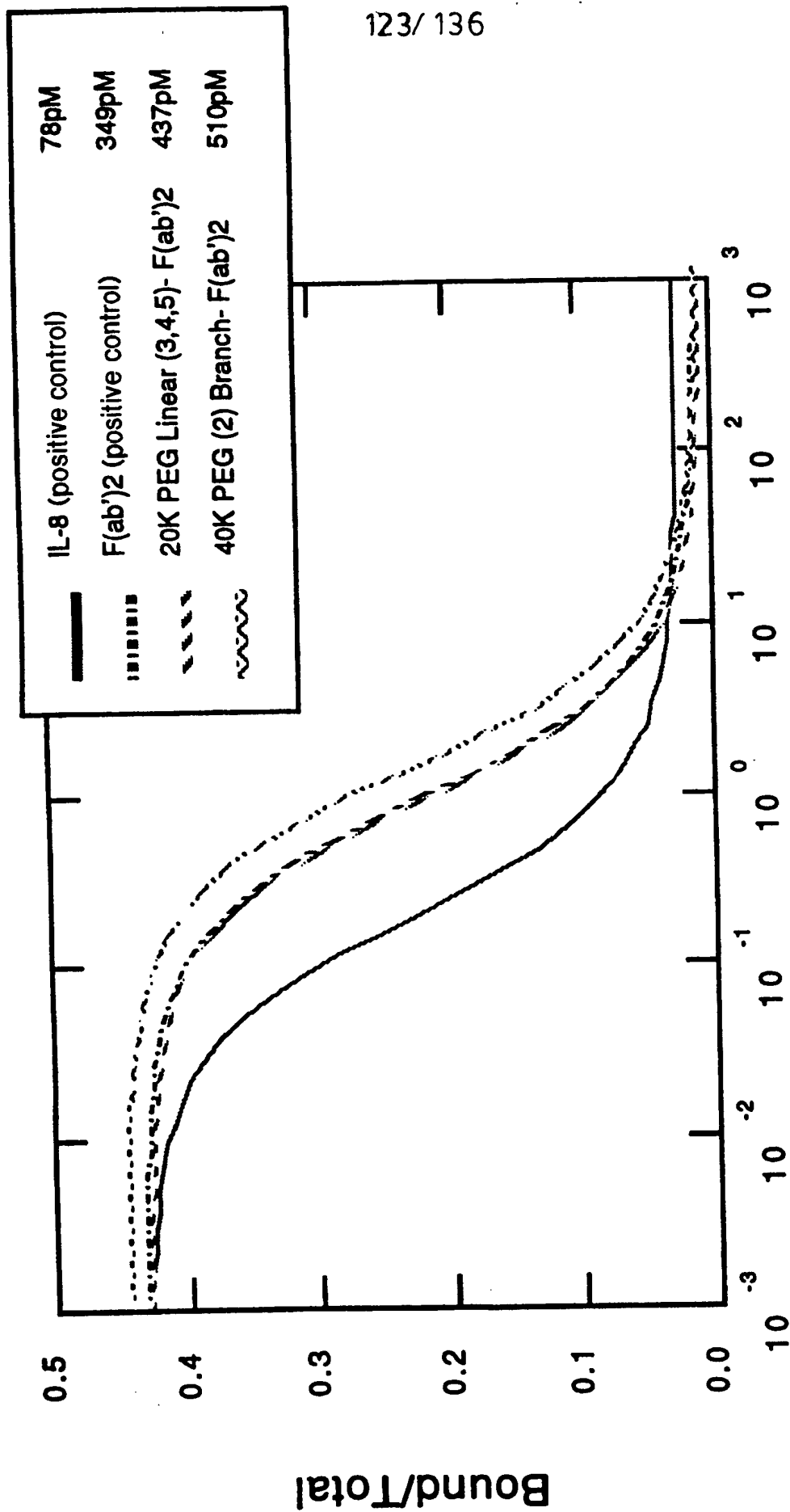
Pegylated F(ab')₂ (nM)

FIG. 57B

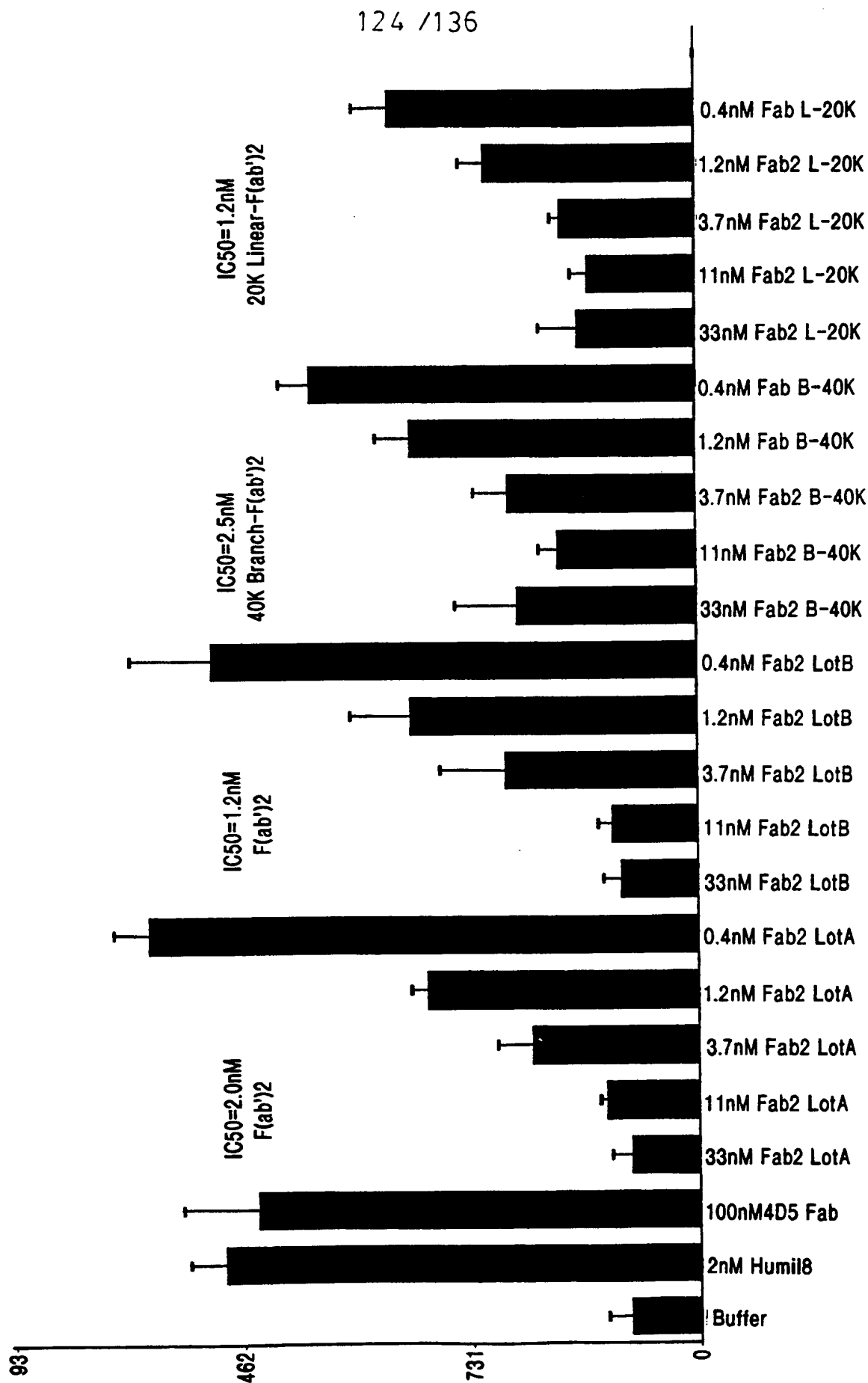


FIG. 58A

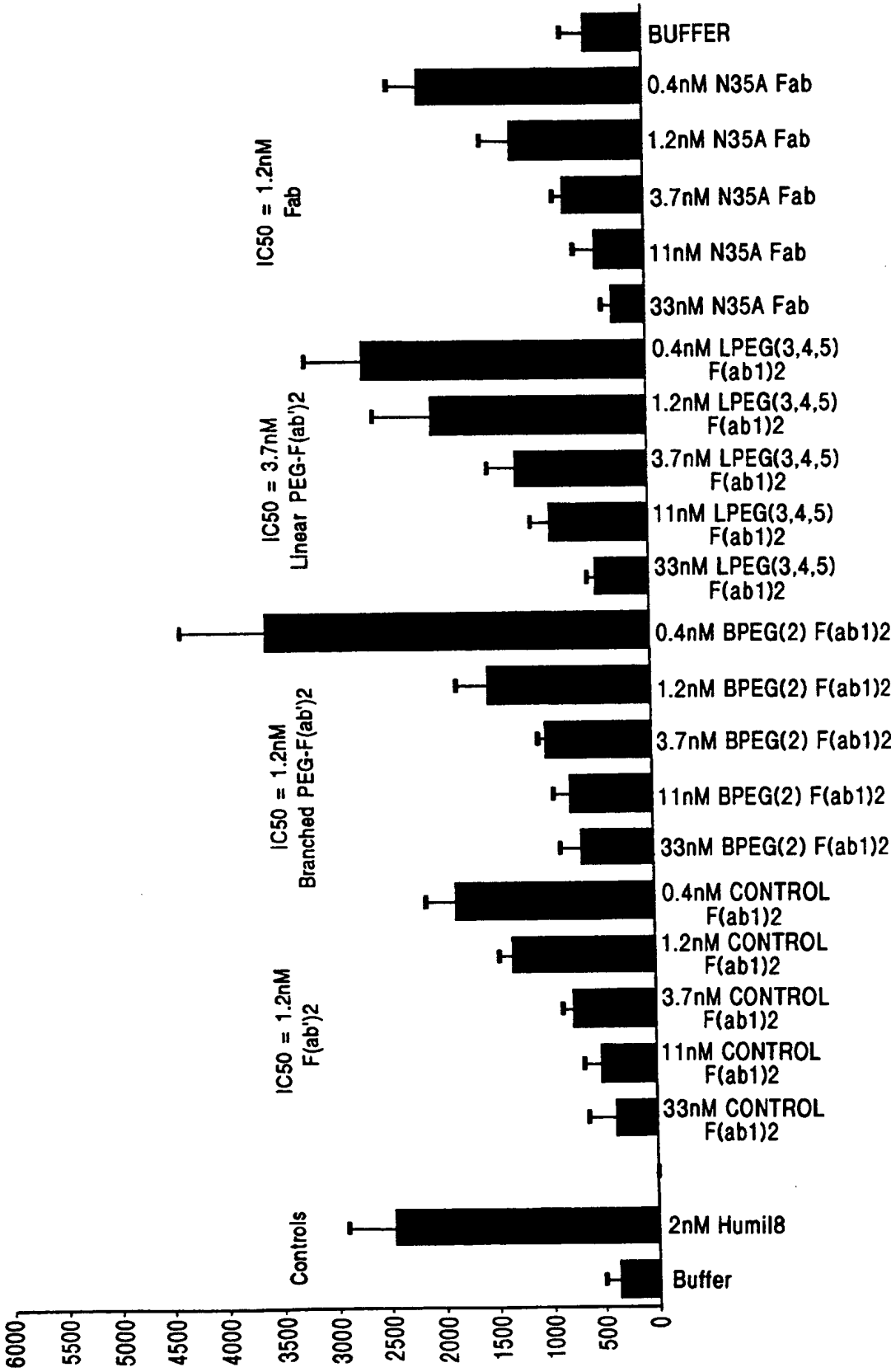


FIG. 58B

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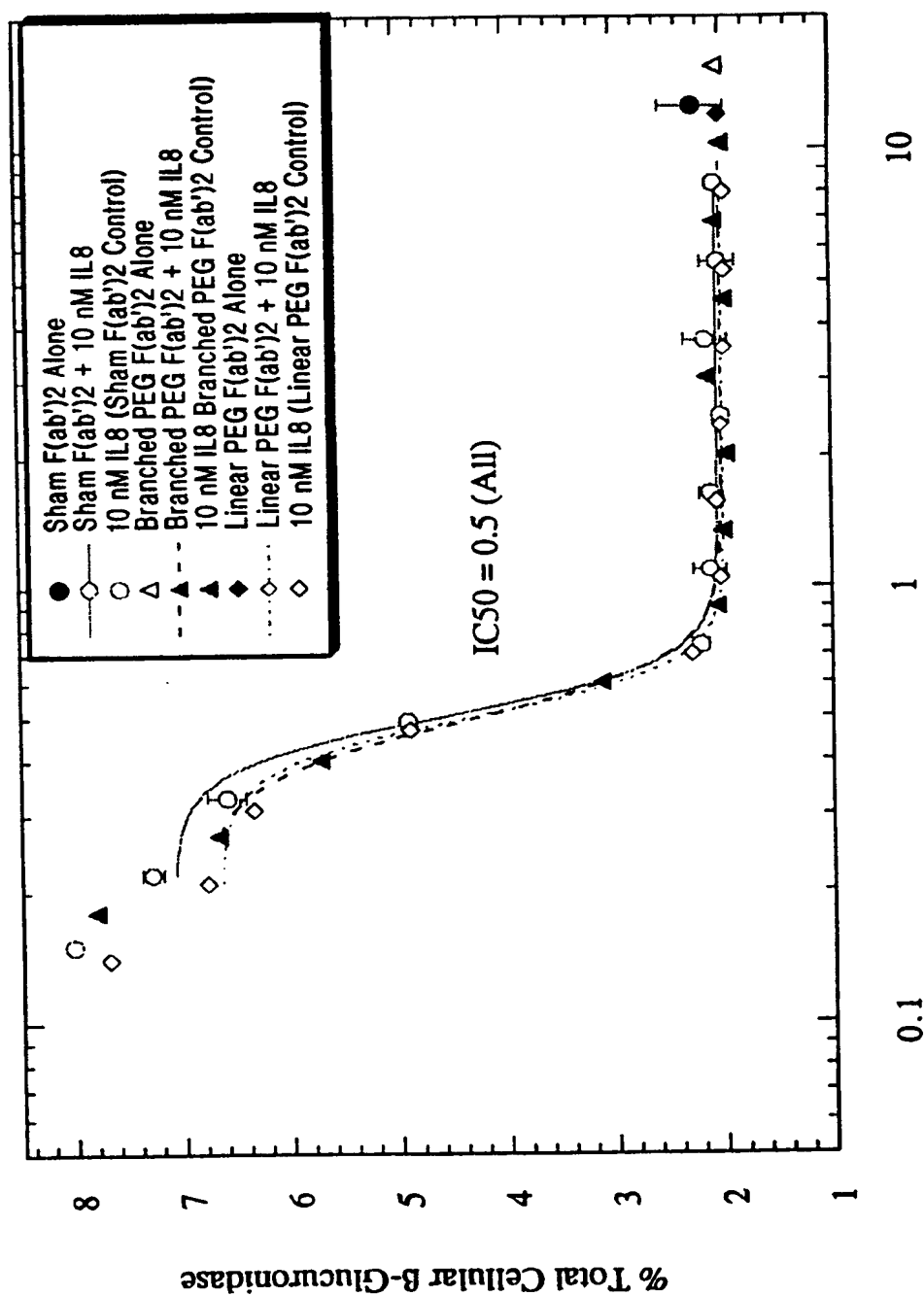
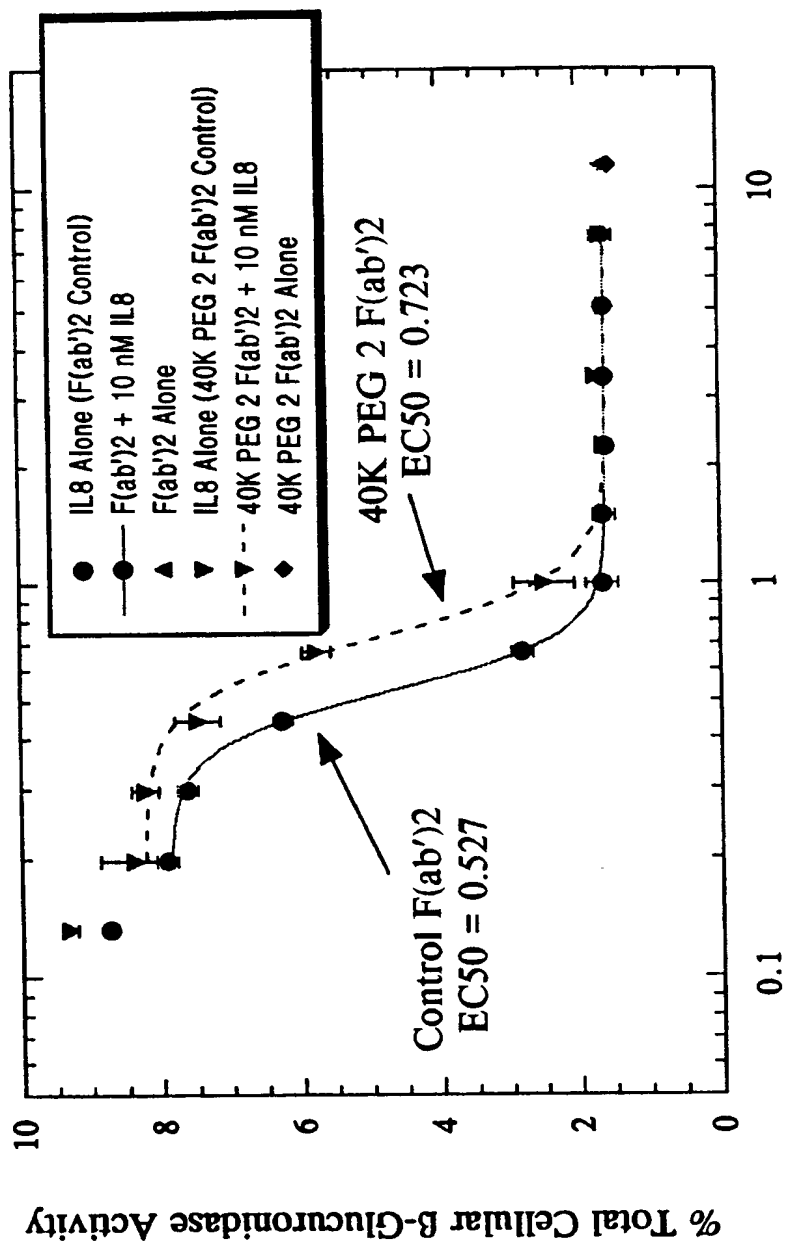


FIG. 59A

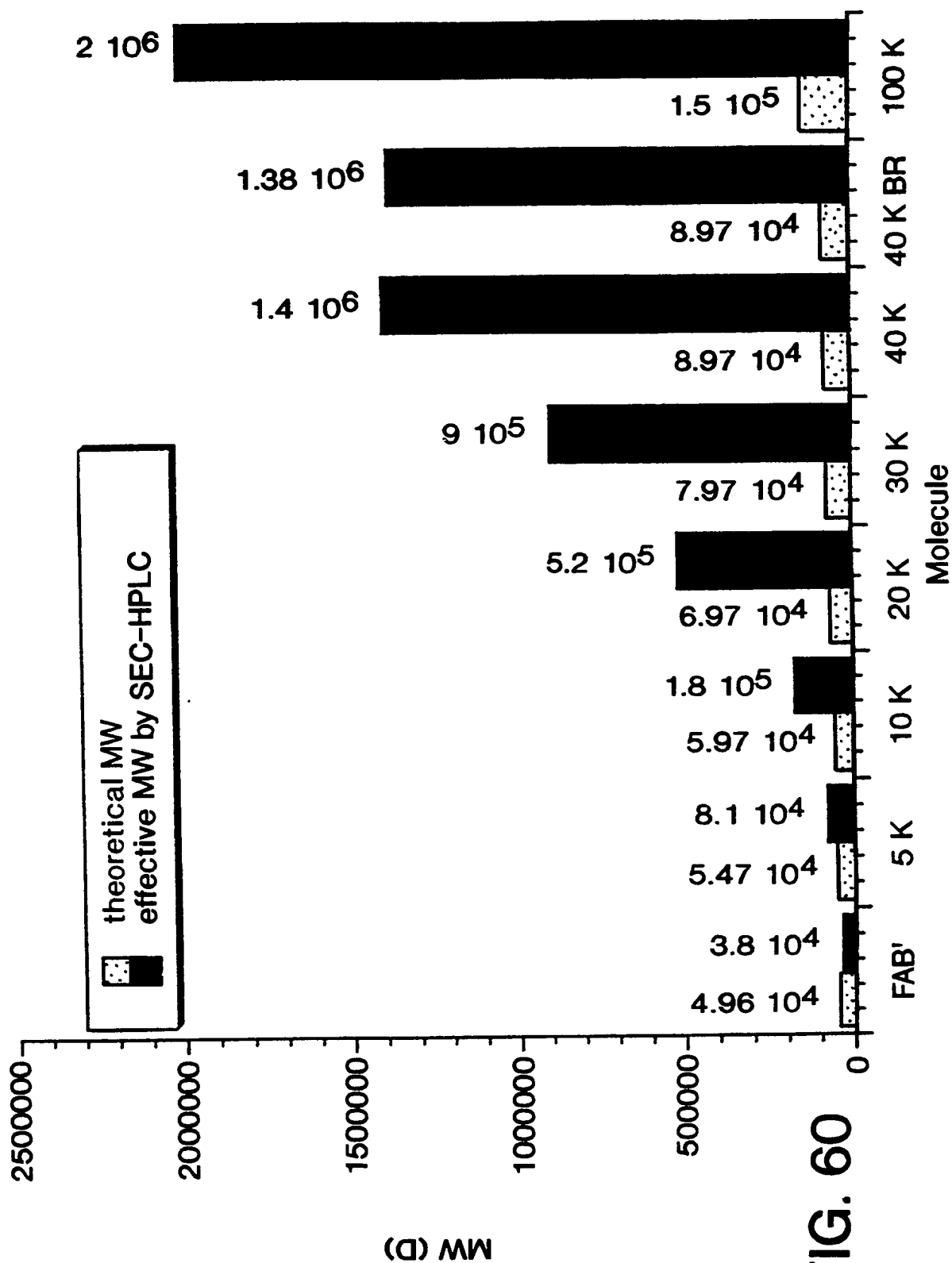
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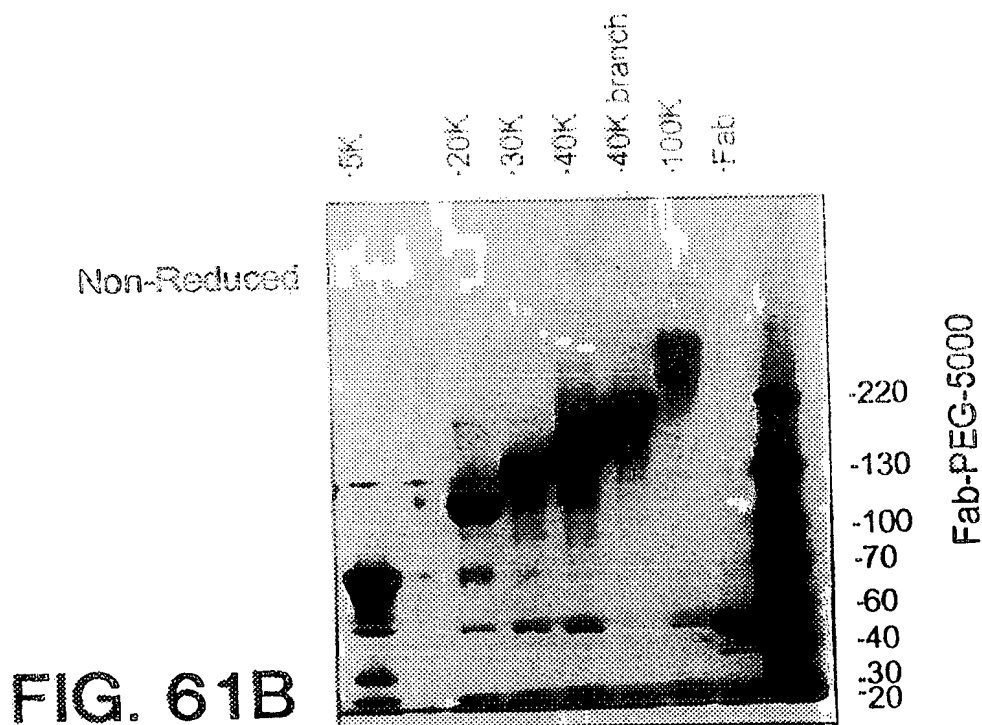
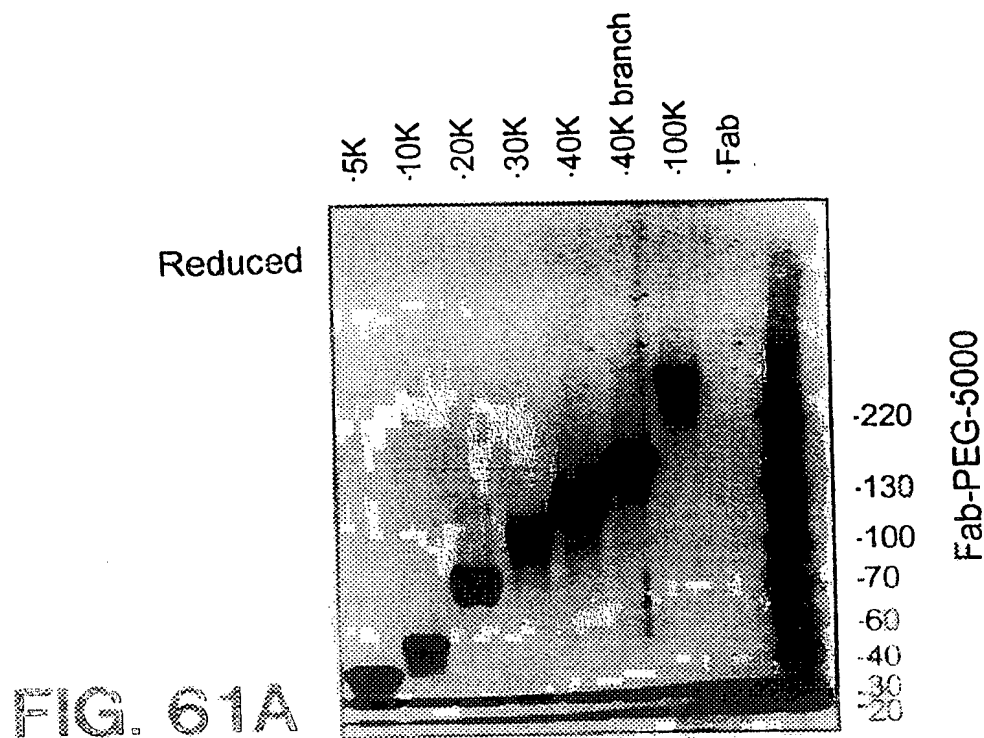


Molar Ratio Antibody:IL8

FIG. 59B

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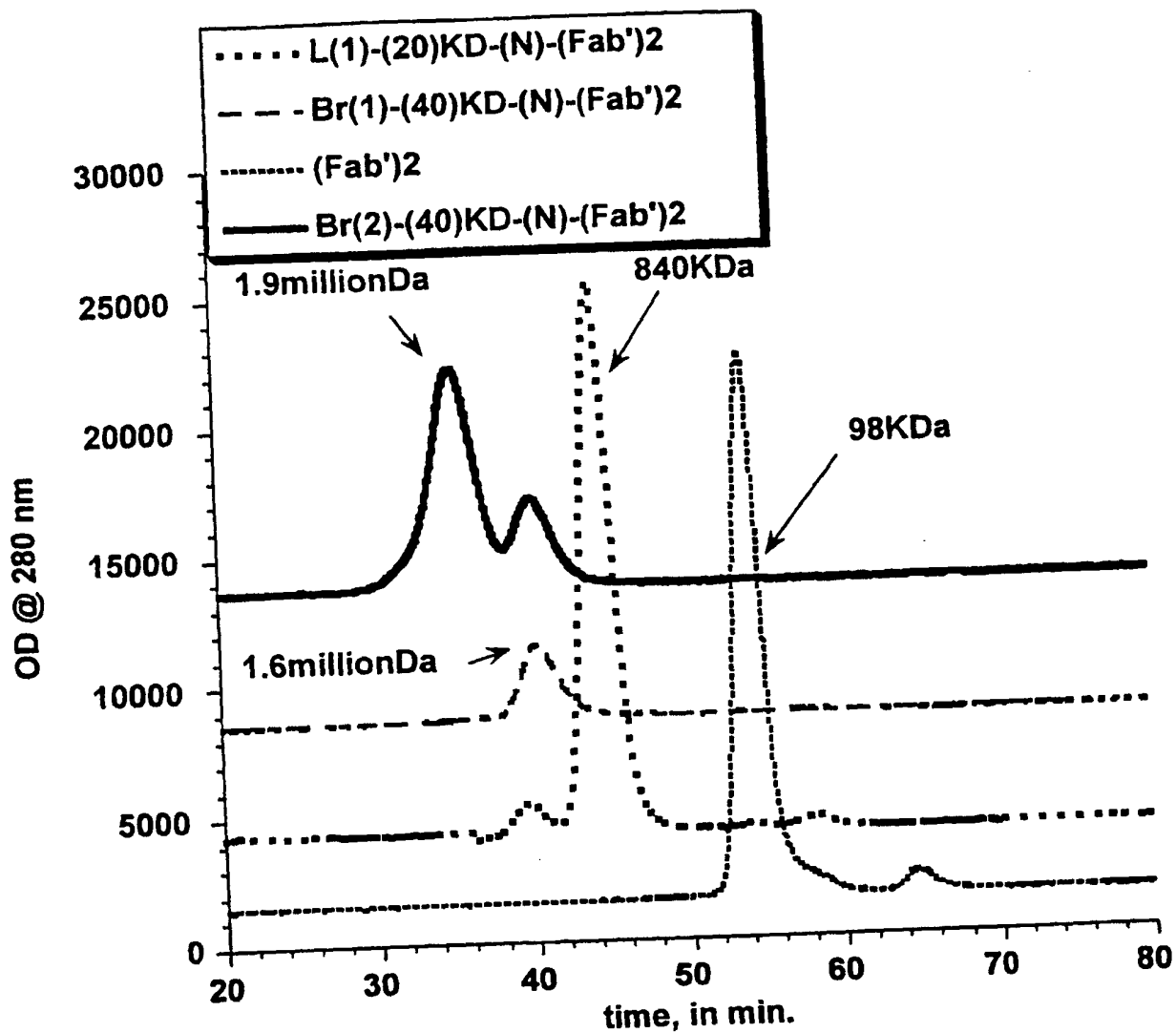


FIG. 62

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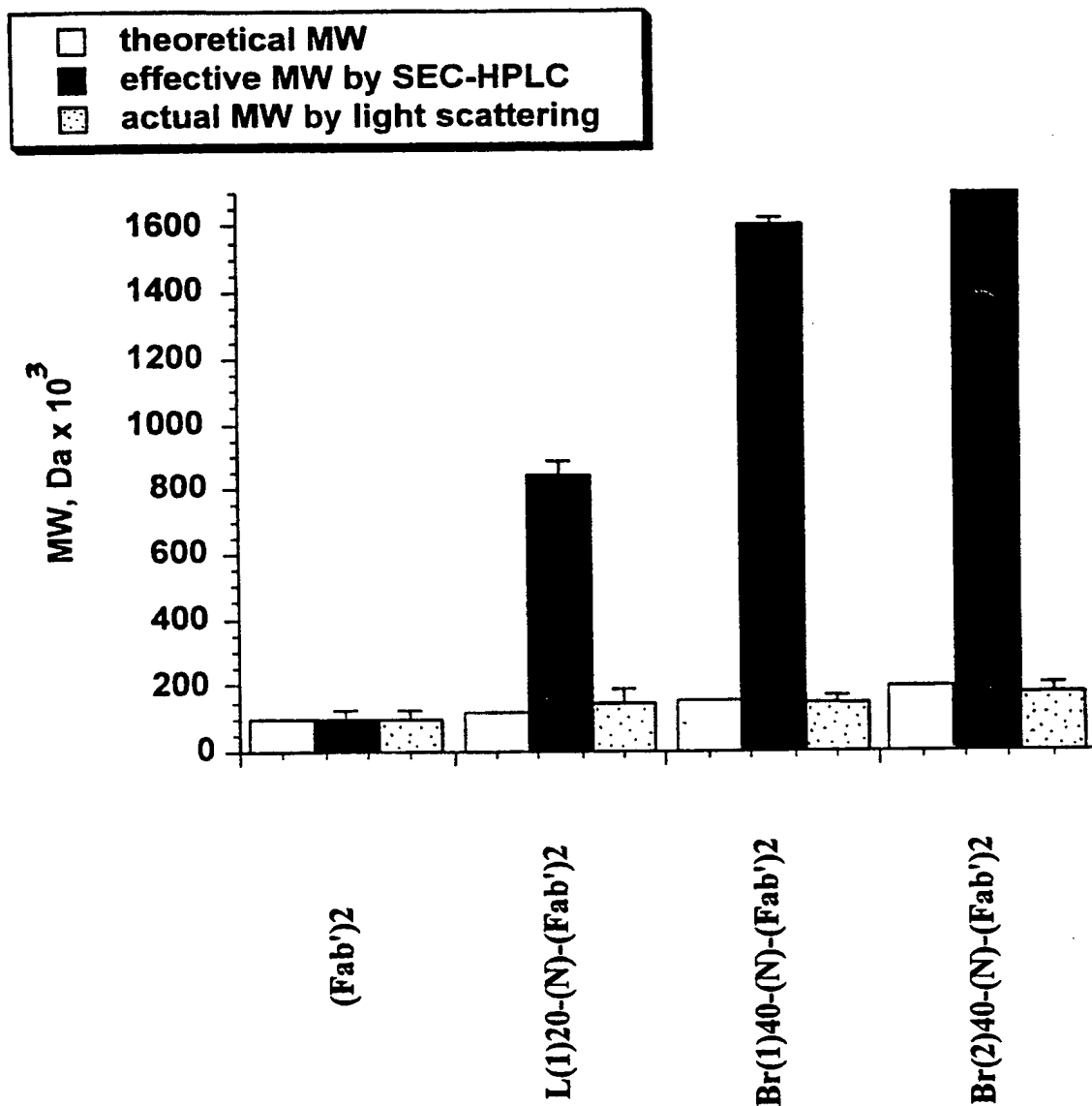


FIG. 63

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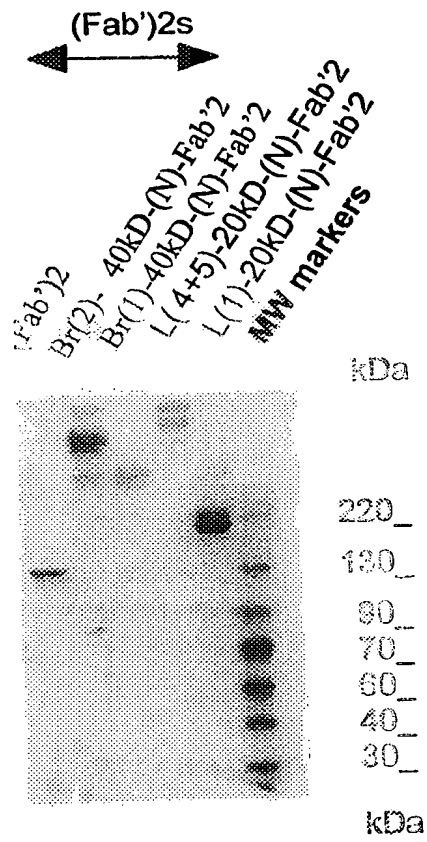
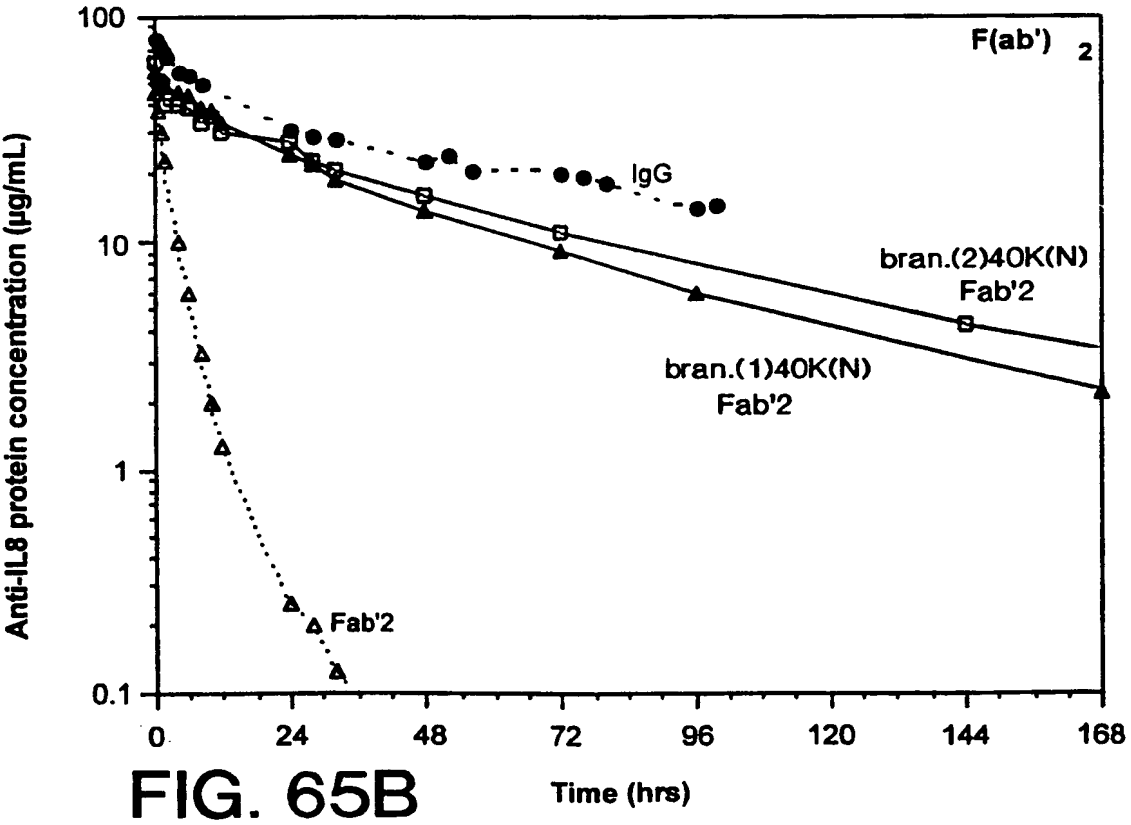
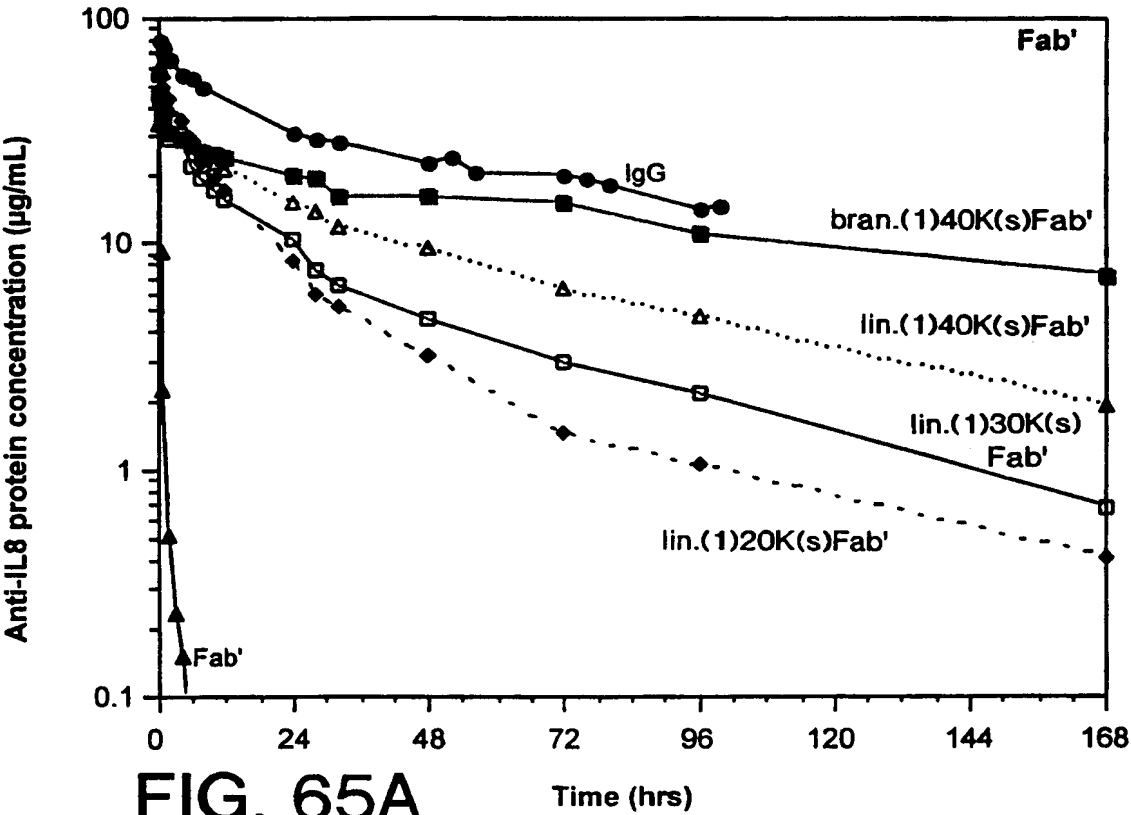


FIG. 64



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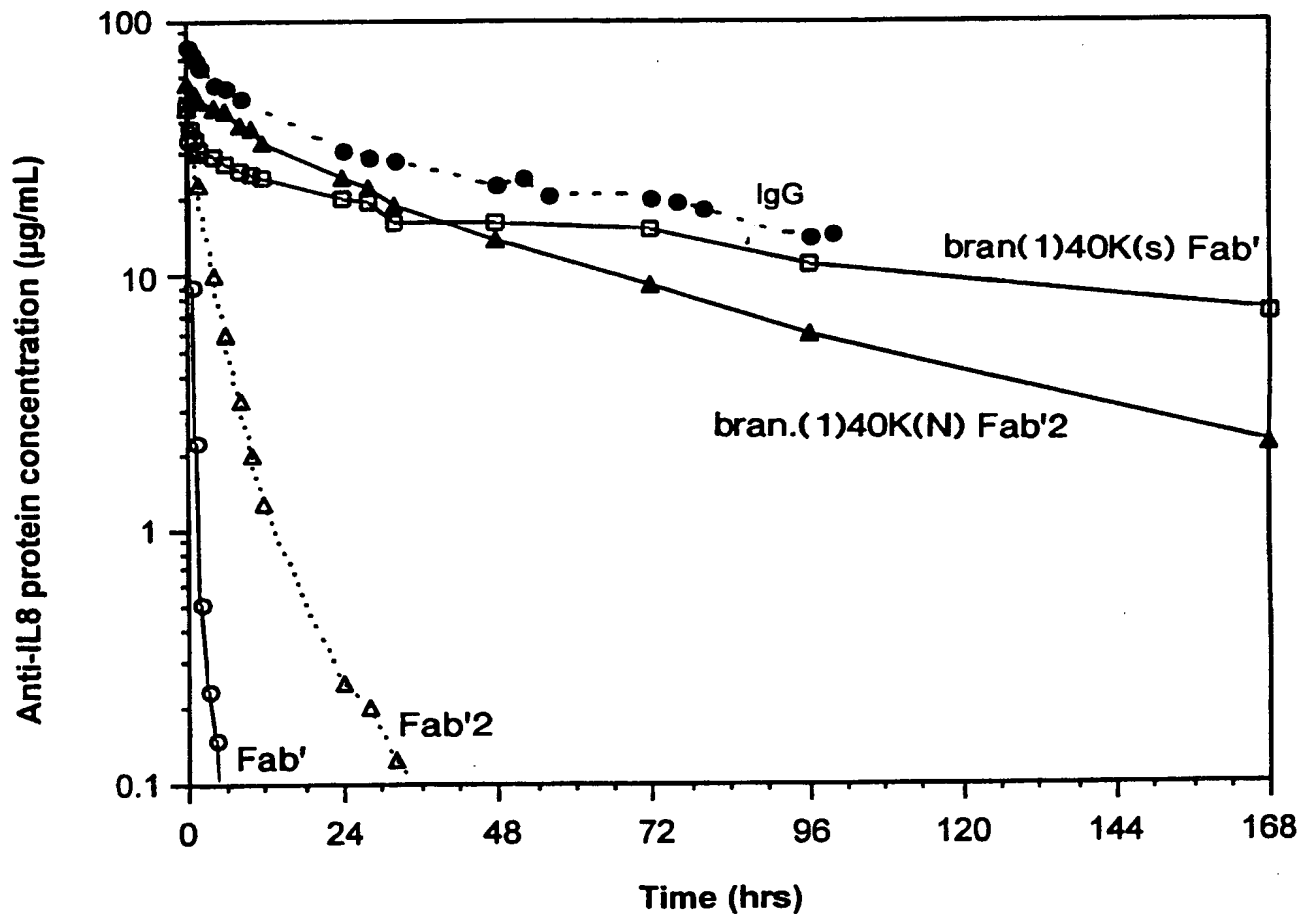


FIG. 66

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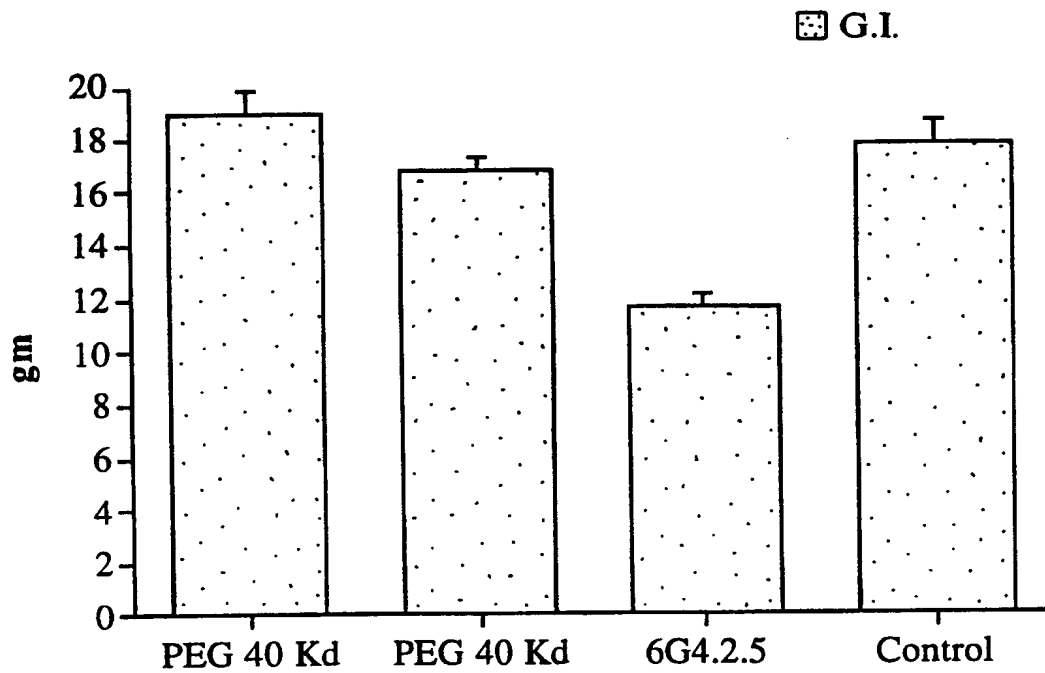


FIG. 67

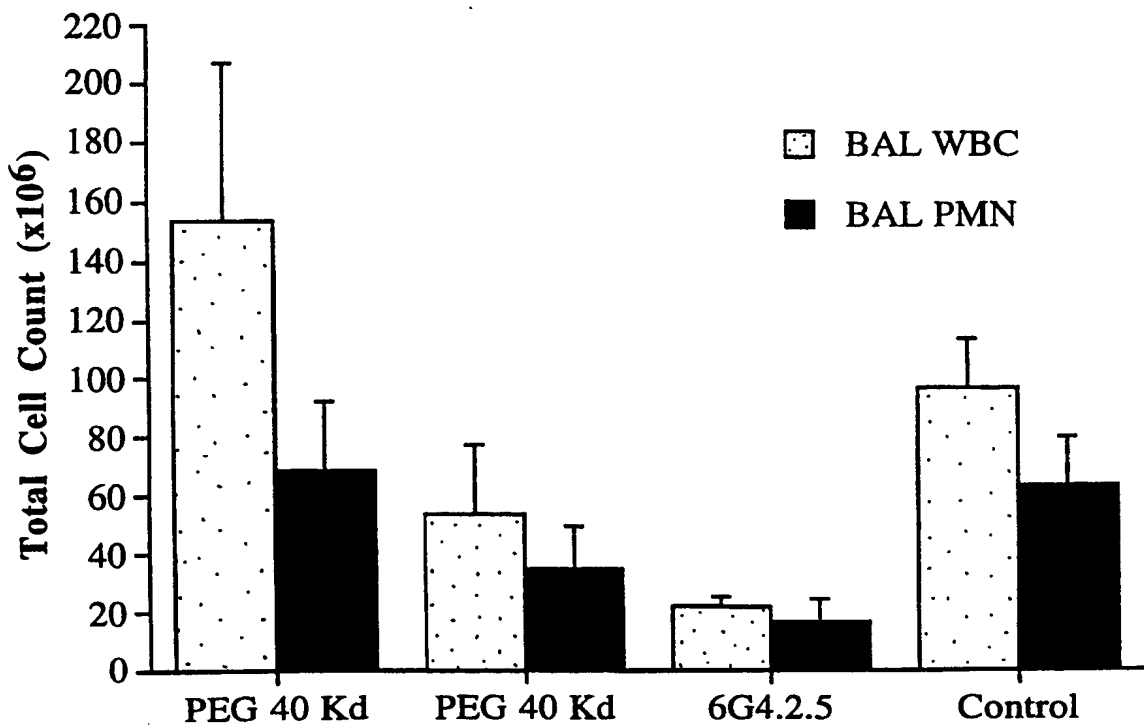


FIG. 68

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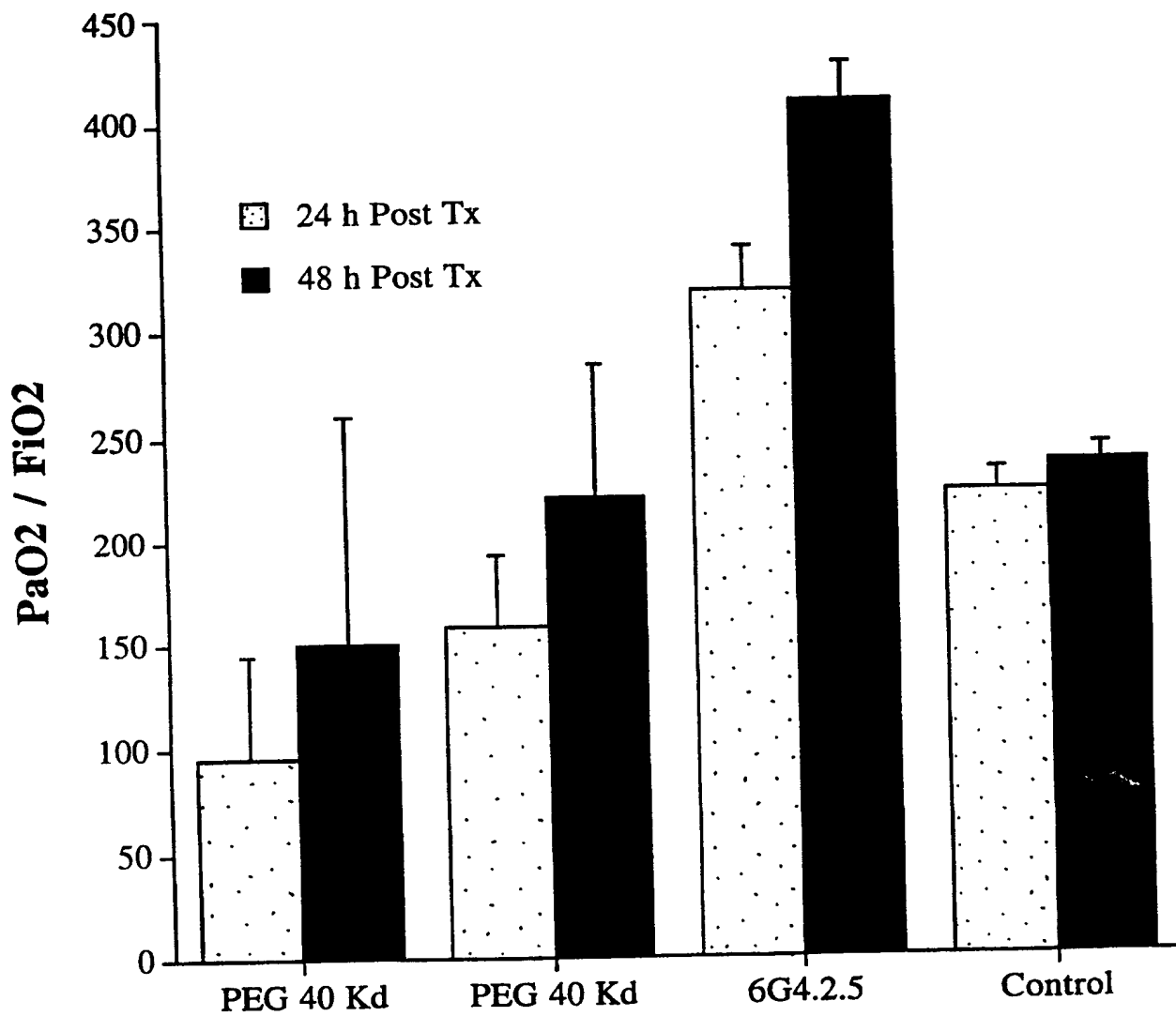


FIG. 69